SEQUENCE LISTING

(110) Zyskind, Judith
Ohlsen, Kari L.
Trawick, John
Forsyth, R. Allyn
Froelich, Jamie M.
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Xu, H. Howard

(120) GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN ESCHERICHIA COLI

(130) ELITRA.001A

(140) 485

(141) FastSEQ for Windows Version 3.0

(210) 1
(211) 159
(212) DNA
(213) E. Coli

(400) 1
caggtggtat ggaaaccaaa aatggagacg ggaagctgaa ccagatagtt actggaggtg 60
atcaccaagca gatgaaataa cgataaccag aacaacgcct tatagcgttg agtttgcgag 120
aaaacgttca tattgtaact ttttgattaa ccattgggg 159

(210) 2
(211) 696
(212) DNA
(213) E. Coli

(220)
(221) misc_feature
(222) (1)...(696)
(223) n = A,T,C or G

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gtcacctact caaacgtgga accgagcgat ttcgttcaga ccttctcacg ccgtaatggt 180
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cgttactncg gctttgtgcc ngaagcgaat ctggtcggtc nggcaacggc tatctggatg 480
aacttcgata accaagaagg cgaatggccg aatggtctgc cctaantcgc attggcgnnt 540
cnttantan ccactttctt cnctttgtcc cttatggca acacttaatt tattntaaan 600
taatcnncg tggctnacaa atccccgcct ttttntaaaa atttccccna anttaaggtt 660
ggcctcngt tgcccgnccc aaacactttg gncccc 696

(210) 3

<211> 681
<212> DNA
<213> E. Coli

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<222> (1)...(681)
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acgtaagcgg atggagtggc cggaaacctc atagtgaccg cccaccagtt ggcctgcatc 180
gctttgtagc gtacgcgcgg cattggcaat aagattcaga tactcagact cttccggggc 240
cttcgccagc atcaaaagagg aggatgctcg cgtatgcagc aactgctcca gcgcaaattg 300
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aaatatttcc tgatagctat cggtatcagg aaccaggtca cgccatgcaa gtttcgtaat 420
ggtcaaactt gatgtttttt agtctgttgt caaagccgcn attataccng taaccggcac 480
tacagcccag gtagaaagca ccgacaaata ctcctggcat gggcgttaaa gctcacagga 540
tggagatctt ttcttcactg gcctaaaaag ctgatattct gtaaagagtt acacngtaac 600
attgagatcg ctatgaaata tcaacaacct ggaaaatctt gnaaagcngg ttggaaaatg 660
gaaagtatcc ggttaagaag c 681

<210> 4
<211> 289
<212> DNA
<213> E. Coli

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tacttaacgg agaacgatta agccttagga cgttcacgc catacttgga acgagcctgc 180
ttacggtcct taacgcgcga gcagtcaagc gcacgacgta cggtgtggta acgaacaccc 240
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<210> 5
<211> 815
<212> DNA
<213> E. Coli

<220>
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<223> n = A,T,C or G

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atatggccgc ctttttcact tttatatctg tgcggtttaa tgccgggcag atcacatctc 180
cgaggatttt agaatggctg aaattacccc atccctggta aaagagctgc gtgagcgtac 240
tggcgaaggc atgatggatt gcaaaaaagc actgactgaa gctaacggcg acatcgagct 300
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tgctgctgat gggctgatca aaaccaaaat cgacggcaac tacggcatca tttctggaag 420
taactgccag actgacttcg ttgcaaaaga cgctggtttc caggcgttcg cagacaaagt 480
tctggacgca gctgttgctg gcaaaatcac tgacgttgaa gttctgaaag cacagttcga 540
agaagaacgt gttgcgctgg tagcgaaaat tggtgaaaac atcaacattc gcggcgttgc 600
tgcgctggaa ggcgacgttc tgggttctta tcagcacggt gcgcgtatcg gcgttctgg 660

ttgctgctaa aagcgctgac gaagaactgg ttaaacacat cgttttgacc tttgttgcaa 720
gccaagccag aattcagaga aactttccgc ttcaccggag gtcccaccca cangganccc 780
cgattttntc agcatggtgg tcttcctncg gagtt 815

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<211> 403
<212> DNA
<213> E. Coli

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cgatagaaac aagcattgaa aggcacagca gtagtcaaac agtgtgaaac gctactggcg 180
ctttacagcg caaaaaggct ggtgactaaa aagtcaccag ccatcagcct gatttctcag 240
gctgcaaccg gaagggttgg cttatttaac ttcaacttca gcgccagctt cttccagagc 300
tttttcagtg gcttctgcgt cgtctttgct cacgccttct ttcagagcag ccggtgcaga 360
ttctaccagg tctttagctt ctttcagacc caggccagtt gcg 403

<210> 7
<211> 149
<212> DNA
<213> E. Coli

<400> 7
gagctttttc agtggcttct gcgtcgtctt tgctcacgcc ttctttcaga gcagccggtg 60
cagattctac caggtcttta gcttctttca gacccaggcc agttgcgcca cgtactgctt 120
tgataacagc aactttgtta gcgccagca 149

<210> 8
<211> 742
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(742)
<223> n = A,T,C or G

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ggacgtcctg tcgcagtata ttaagtcgtc gatagaaaca agcattgaaa ggcacagcag 180
tagtcaaaca gtgtgaaacg ctactggcgc tttacagcgc aaaaaggctg gtgactaaaa 240
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tcaacttcag cgccagcttc ttccagagct ttttcagtgg cttctgcgtc gtctttgctc 360
acgccttctt tcagagcagc cggtgcagat tctaccaggt ctttagcttc tttcagaccc 420
aggccagttg cgccacgtac tgctttgata acagcaactt tgttagcgcc agcagctttc 480
agaattacgt cgaattcagt tntttcttca gcagcttcaa ccgggccagc agctacagct 540
acagcagcac caagcggaaa caccgaattt ttcttccatt gcagagatca gttctacaac 600
cgtccattac agacatagct gcaactgctt caatgatttt gatctttagt ggatagacat 660
ttaaattgtt cctgaattat caagaaataa gtnttatacg taagccgaaa tgcgttaaaa 720
aagataactc ngattaaagc ag 742

<210> 9
<211> 421
<212> DNA
<213> E. Coli

<400> 9
agtagtnaaa cagtgtgaaa cgctactggc gccttacagc gcaaaaaggc tggtgactaa 60
aaagtcacca gncatcagcc tgatttctca ggctgcaacc ggaagggttg gcttatttaa 120
cttcaaattc aacgccagct tcttccagag ctttttttag tgcttctgcg tcgtctttgc 180
tcacgccttc tttcagagca gccggtgcag attctaccag gtctttagct tctttcagac 240
ccaggccagt tycgccagct actgcttttga taacagcaac tttgttagcg ccagcagctt 300
tcagaatttc gtcgaattca gttttttctt cagcagcttc aaccgggcca gcagctacag 360
ctacagcaac agcagcggaa acaccgaatt tttcttccat tgcagagatc agttctacaa 420
c 421

<210> 10
<211> 106
<212> DNA
<213> E. Coli

<400> 10
agagcttttt tcngtgcttc tgcgtcgtct ttgctcacgc cttcttttag agcagccggt 60
gcagattnta ccaggtcttt agcttctttc agacccaggc cagttgcgcc acgtactgct 120
ttgata 126

<210> 11
<211> 262
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(262)
<223> n = A,T,C or G

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ctgcaacccg aagggttggc ttatttaact tcaacttcag cgccagcttc ttccagagct 60
ttttcagtgg cttctgcgtc gtctttgctc acgccttctt tcagagcagc cgntgcagat 120
tctaccaggt ctttagcttc tttcagaccc aggccagttg cgccacgtac tgcttttgata 180
acagcaaccc tgttagcgcc agcagcttcc agaattacgt cgaattcagt ttttcttcca 240
gcagctttaa ccaggccagc ag 262

<210> 12
<211> 202
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(202)
<223> n = A,T,C or G

<400> 12
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gtaggtggtg ttaccggtgn tcagatccgg gaagatgaac acggtagcgc gacctgcaac 120
cggagagttc gcggctttgg attncgcaac gtcagccatt accgcagcgt cgtactgcag 180
cggaccggcn atccatcaggt ca 202

<210> 13
<211> 261
<212> DNA

<213> E. Coli

<400> 13
tctaggaatt agaatagctt caaattcagc agttgacagt ggcataaacg taactggtga 60
cttttgcccg gcatgacgcc gggcttttct tattattccg tgacttccag cgtagtgaag 120
gcaaacttct cgtccatcaaa tagcccctga ctggttagtt ttagcgcggg gatcactggc 180
agagaaaaga acgccatctg aataaacggc tcatcgggta acggacccca ttcacgggcg 240
gcgggttttc aggcgtcaat t 261

<210> 14
<211> 334
<212> DNA
<213> E. Coli

<400> 14
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ttttattat tatggggaag gtgttattta tgagtttcat ttatgccgta acgacaatga 120
actcgggaat tattataagc agcgcgagaa taataatcat tgtgcaaatg ctaattttaat 180
taatactatt taaatattat tttgagcata tgcacataag gttg 224

<210> 15
<211> 342
<212> DNA
<213> E. Coli

<400> 15
aattccgttc ttttttcgt caacggtgtc cagaatcatt ttatttacct cgggtactta 60
tgctgatttt tattattatg gggaaggtgt tatttatgag tttcatttat gccgtaacga 120
caatgaactc gggaattagt ataagcagcg cgagaataat aatcattgtg caaatgctaa 180
tttaatttat attatttaaa tattatttg agcatatgca cataaggttg gg 242

<210> 16
<211> 312
<212> DNA
<213> E. Coli

<400> 16
aatagcgggt atgcacgcct ttctttttct cgtcaacggt gtccagaatc attttattta 60
cctcgggtac ttatgctgat ttttattatt atggggaagg tgttatttat gagtttcatt 120
tatgccgtaa cgacaatgaa ctcgggaatt agtataagca gcgcgagaat aataatcatt 180
gtgcaaatgc taatttaatt aatactattt aa 212

<210> 17
<211> 433
<212> DNA
<213> E. Coli

<400> 17
cctttgtaaat tatcgccgct ggcataaaaa ctgcgtccaa acgccgtctt tgccagcagc 60
caggccataa atgccaccag aattatcgtc aaccaaccaa ttgctgaaac gccaagcagc 120
agcgggcggg acaagctgttt cagttcggcg ggtaacgctt caatccattt gccgccagtc 180
cacagcaaca tgatgcctct gtacaacgct aacgtgccaa gggtggcaac aatggcaggg 240
atctttatgcc acgcgacgag gacacgcgttg aaaaatcccg cgagcaaacc aagcagtaaa 300
gtcgcgacac aagcaacagg tagtgaatat cctgcgttca gtaacatccc caacagcacc 360
gcgcacattc cggtaatcga acccactgaa acatcaatat tgcgcgtaag cattaccagc 420
gtcgcgccca ttg 433

<210> 18
<211> 668
<212> DNA
<213> E. Coli

<400> 18
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tcttccctcg ttgaggacac cgggttgtca ggttgaccat acgcttaagt gacaaccccg 120
ctgcaacggc ctctgttatc aattttctgg tgacgtttgg cggtatcagt tttactccgt 180
gactgcttcg cagccctttt taaagtgaat tttgtgatgt ggtgaatgcg gctgagcgca 240
cgcggaacac ttaaaaccaa aaacagtgtt atgggtggat tctctgtatc cggcgttaat 300
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acgggaggtt ttaaaataaaa tatgcattgt ttcaatgctg gctcgtttac gtctgatgcc 540
aaaaggatgt gtacaatgaa ttcagcattt gtgcttgttc tgacagtttt tcttgttttc 600
ggagagccag ttnatattgc agtcaagtgg tcacaggaca atgcaggagt gtatgact 658

<210> 19
<211> 598
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(538)
<223> n = A,T,C or G

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attgttaatt ggttaacgtc acctggaggc accaggcact gcatcacaaa attcattgtt 180
gaggacgcga taatgaaaac gttattacca aacgttaata cgtctgaagg ttgttttgaa 240
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gaacgggagg tattaaataa aatatgcatt gttcaatgc tggctcgttt acgtctgatg 360
ccaaaaggat gtacaatgaa attcagcat ttgtgcttgt ctgacagttt tttcttgttt 420
cggagagccg agttgatatt gcagtcagtg ttcacaggac aatgcangag tgtatgactg 480
cagcaatccg aacagaaaat tcccggtaac tgttacccgg tcgataaagt tattcaccag 540
gataatattg aaatcccggc aggtctttaa aacagttccg taataaat 598

<210> 20
<211> 191
<212> DNA
<213> E. Coli

<400> 20
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ctgaccttta ttgcaataa gcacgccatt agcgtcatag a 101

<210> 21
<211> 446
<212> DNA
<213> E. Coli

<400> 21
tcgcgtgttt acctcaaca tcggtaactt tctggcggat agtttcacgg taagcaacct 60
gcggtttacc tacgttcgct tcaacgttga attcacgctt catacggtca acgatgatgt 120

cgaggtgcag ttcgcccata cccgcgatga tggtctggtt agattcttcg tcagtccata 180
cacggaaaga cgggtcttct ttagccagac ggcccagagc cagacccatt ttttcctggt 240
cagctttggt tttcggttca actgcgatgg agattacggg ctcagggaat tccatacgtt 300
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cgatagcagc atcgatgtcg cccgcgcgaa ctttcttgat ctcttcacgt ttgttagcgt 420
gcatctgaac gatacgaccg aaacgctcac gtgcagcttt cacgg 465

<210> 22
<211> 859
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(859)
<223> n = A,T,C or G

<400> 22
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cagccagttt aatcgccagt tcagaggagt caacgtcatg gtaagaaccg aagtgcagac 120
gaatacccat gtctactacc gggtagcctg ccagcggacc tgctttcagc tgttcctgga 180
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tgaactcgta gcctttcggg tttgaacccg gctccagcgg gtacatgtcg ataacaacat 300
gaccatactg acgacgacca ccagactgtt tcgcgtgttt actttcaaca tcggtaactt 360
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anggngtacc acnggggtac ntntttttaa nancgattgc cagcancgga tntnncccgn 720
gccnaacttc tttggaacnn tttaccggtt ggtaaccngc cttttnaacn atccaaccga 780
aaaagngtta anngccantt ttccnggngt tnanntncgg nttcccngaa ntaacccncc 840
cggggtnaac ccngnaaaa 859

<210> 23
<211> 269
<212> DNA
<213> E. Coli

<400> 23
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agtcaacgtc atggtaagaa ccgaagtgca gacgaatacc catgtctact accgggtagc 120
ctgccagcgg acctgctttc agctgttcct ggataccttt atcaacggcc gggatgtatt 180
cgccagggat tacaccacct ttaatgtcgt tgatgaactc gtagcctttc gggtttgaac 240
ccggctccag ccagtacatg tcgataaca 269

<210> 24
<211> 530
<212> DNA
<213> E. Coli

<400> 24
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atgactcatt gccgatacct gattaaacgg gtcatcaaaa tcatcattgc tgttttacag 120
ctgatcattc tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt 180
cggacgcacc tttaataact ataaataagt gtctgggcag atactatata aattaactta 240
gtgaatgatt atgctaatgt catcaattaa ataaatataa tggcgttaag gcttcccagt 300

aatataatta atactctact tccagagtag 330

<211> 25
<211> 471
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(471)
<223> n = A,T,C or G

<400> 25
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atgactgatt gccgataccc gattaaacgg gtcatcaaaa tcatcattgc tgttttacag 120
ctgatcctcc tgttcttata acacaaggaa acgtacttaa ggtgccgtcc ggtgaaccag 180
tcggacgcac cttaataac tataaataag tgtctgggca gatactatat aaatttaact 240
agtgaatgat tatgctaatg tcatcaatta aataaatata atggcgttaa ggcttcccag 300
taatataatt aatactctac ttccagagta gaatattaaa ttttatccgc gtggtgcatc 360
agcacaaatt tatcccacaa ctgttcttct gtctcgacat gccccccgat ctttnacaaa 420
tantattggg ggattnggcc cncctttttg ncaggttggg gtcntctnat g 471

<211> 26
<211> 379
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(379)
<223> n = A,T,C or G

<400> 26
natctgantg gttgccattcc ttgtttaagg aaaccctgaat gactgattgc cgatacctga 60
ttaaacgggt catcaaaatc atcattgctg ttttacagct gatccttctg ttcttataac 120
acaaggaaac gtacttaagg tgcgtccggt gaacgcagtg gacgcacctt taataactat 180
aaataagtgt ctgggcagat actatataaa ttaacttagt gaatgattat gctaatgtca 240
tcaattaaat aaatataatg gcgttaaggc ttcccagtaa tataattaat actctacttc 300
cagagtagaa tattaaattt tatccgcgtg gtgcatcagc acaaatttat cccacaactg 360
ttcttctgtc tcgacatgc 379

<211> 27
<211> 749
<212> DNA
<213> E. Coli

<400> 27
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caaaaacaac taaatcaaaa aataatggca ttagaaaata taatgcgaaa acggaggtga 120
aattagttta tttcaaaatga ggaaaatctc ccggcgaaaa aacgggaga tgaaagtgtg 180
atgggtatca aatgaaacaac agaggagaaa tttttaacgc agccattcag gcaaatcgtt 240
taatcccatt gcctggcgga taagttgcgg cttaacgcca ggaagcgtgt cggccagttt 300
caaaccaata tcacgcagca gttttttcgc cggattggta ccggaaaaca gatcgcggaa 360
tcgctgcata ccacgccagca tcaacgccgc actgtgcttg cggctacgct catagcgacg 420
cagataaatg tattgcccga tgtctgggat ccgtcgacct gcagccaagc ttgggctttt 480
cagcctgata cagattaaat cagaacgcag aagcggtctg ataaaacaga atttgcctgg 540
cggcagtagc gcggtggtcc cacctgaccc catgccgaac tcagaagtga aacgccgcta 600

gcgcccgatg gtagtgtggg gtctccccat gcgagagtag ggaactgcca ggcatcaaat 660
aaaacgaaag gctcagtcga aagactgggc ctttcgggttt atctggtggt tgtcggtgaa 720
cgctctctga gtaggacaaa tccgccggga gcggattttg aacgttgcga aacaacccgc 780
ccggaaaang gtgggggcct 798

<210> 18
<211> 636
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(636)
<223> n = A,T,C or G

<400> 18
aggggttttg ttttgggcaa tgatgcattt aagttatcgt ctgcagatag aggagatatt 60
acaataaana angaatcagg gcatttgata gtcaataccg caatttctatc aggagatata 120
gtcactctaa gangaggaga aattaggttg gtattatagc ttgtgcgcgc catgattggc 180
gcgcaatttn aactttagtgc tttacatcgc tattgtcttg atttctttga attatttttat 240
aaatttaaaaa aangactgtt atgtataagc aaaggtcgaa cgaaaaatac attccaaata 300
aatgcttgct tnaatctcta tatcctttcc cgaaaaatga cacataaaat tgagatattc 360
caaaaagtgn tnntacaaat aaagatgcct ttatttttatt atttctaata aaaatagaag 420
caataaaaaa tnntaacaat gatataaatc taatgttttt aaatatattg tcttttatgt 480
tagtaatagt cgttagtatg tttgatttcc catattttac gtgtagtttt ttatatacat 540
ggaaattntt ntctttatac tgagacatca cacgatcatc aaatggaagt ttgaagatgg 600
tgcttgnttt gntaacaaat aaaaagagtg catttcg 636

<210> 19
<211> 757
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(757)
<223> n = A,T,C or G

<400> 19
cagcggtcgn attttagca tggtttttta ttggcggcta tgctgccccg ggagcataaa 60
gatgaaaaaa anaacgatta ttatgatggg tgtggcgatt attgtcgtac tcggcactga 120
gctgggatgg tngtaacgtc acctctaaaa aatagcaaag gctgcctgtg tgcagccttt 180
gtgcaatttn aingttaact tttaatcttc ctgtagataa atagcacgac aatcgcacca 240
ataacgnaaa cnnacgaagct gccaaaattg aagccatcga ctttaccaaa gccaaacagc 300
gtgctgatcc angcggcgac tacggcaccg actatcccca gcaggatagt cataaagaat 360
ccacctccat cnttaccgtgg catgatccac ttcgccagaa taccggcaat aagccaaaaa 420
ataatcnatg anagaatgcc cattgtttcc tcacttatct gttttgcatt agcgggttag 480
tcgctgatna aaagcatagc acaacatcgg gagggcaaga tttgtgacga gcatcacgga 540
ggttttttct gcgatggcgc agaaattgcg ccatcaacga tcagtgataa ttaccaacca 600
caaacatcat gttcgttttc cgtgtccataa gaaccgtacg ggattcacca gatcttttat 660
cacttcnagt ccgcacttct ggcaccagca aagtcatcgg cgtctctggt tcataatcga 720
ccggaancgt cattgctggt attggtgacn gtcacgg 757

<210> 20
<211> 502
<212> DNA
<213> E. Coli

<400> 30
aattacagaa aaaggaggca atatcgggta aaggcattag cccgacgaat acgtcgggct 60
acaaatattg ttgtgctgca ggtgttttag cgggttgttg atccacaggt tctaactgga 120
agaccacatc gacctgatca tcaaactgaa tagcggcctg ctcgtaagtt tcctgggcgg 180
acacccggcg ggcatcggct ttcatcatcc gcaccattgg gctgggctga tagttggaaa 240
catggtagcg cacgctatat acggccccca gtttacgatg aaagccgttc gccagttcct 300
gcgcctgatg aatcgcgtta tcaatcgctg ccttacgcgc tttgtcttta taggcatccg 360
gctgcgccac gcccagcgac acagaacgaa tt 392

<210> 31
<211> 351
<212> DNA
<213> E. Coli

<400> 31
ctatccttga tgaaacgcgc agcaaagata ggtgattacg tcatggtttt acagaaaatt 60
acagaaaaag gaggcaatat cgggtaaagg cattagcccg acgaatacgt cgggctacaa 120
atattattgc gctgcaggtg ttttagcggg ttgttgatcc acaggttcta actggaagac 180
cacatcgacc tgatcatcaa actgaatagc ggcctgctcg taagtttcct gggcggacac 240
ccggcgggca tcggctttca tcatccgcac cattgggctg ggctgatagt tggaaacatg 300
gtagcgcacg ctatatacgg ccccagttt acgatgaaag ccgttcgcca g 351

<210> 32
<211> 762
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(762)
<223> n = A,T,C or G

<400> 32
aattatgaaa cactgtctgg aatcgtctga atgacgggca catttgcgag cacgcatcca 60
gtaataacac aggaaactat tttatctacg cgttagcgat agactgcttg catggcgaaa 120
ggaggtaagc cgacgatttc agcgggacgc tgaaacggga aagcccctcc cgaggaaggg 180
gccataaata aggaaagggt catgatgaag ctactcatca tcgtggtgct cttagtcata 240
agcttctccg cttactaaga ctaccagggc ggggaaaccc ccgctctacc ctcactcctg 300
aaagtatgcc ttcacgataa gattgtcaat ccgcaggctt tgtagtctgc gatcctgcca 360
gcaaatattc tttgccagtc gttacgcaat aatcacagag gaaactattt tattcacgcg 420
ttagcgattg actgcattca gggcgaaagg aggtaagccg atgatttcag cgggacgctg 480
aaacggaaag gcctctcccg gagaagaggg cttttaataa ggaaagggtt atgatgaagc 540
acgtcatcat actggtgata ctcttagtga ttagcttcca ggcttactaa gaacaccagg 600
gggaggggga aacctcttcc taaccctcac ttctgaaatt gggtgctatg acgctggcgt 660
tactgcttac cgctaccagt ttgtctgccc tggcggttgt aacgccagat cggtacccgt 720
ttggatattt taatgaaagc cgacaaatca atcancgtga cg 762

<210> 33
<211> 283
<212> DNA
<213> E. Coli

<400> 33
gcacatttgc gagcacgcat ccagtaataa cacaggaaac tattttatct acgcgttagc 60
gatagactgc ttgcatggcg aaaggaggta agccgacgat ttcagcggga cgctgaaacg 120
ggaaagcccc tcccgaggaa ggggccataa ataaggaaag ggtcatgatg aagctactca 180

tcatcgtggt gctcttagtc ataagcttcc ccgcttacta agactaccag ggcgggggaa 240
accccgcttt accctcactc ctgaaagtat gccttcacga taagattgtc aat 293

<210> 34
<211> 633
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(633)
<223> n = A,T,C or G

<400> 34
atttacactt tttacgaaat catgggatca ctaacaaaat atcgcttgtc agttatattg 60
tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 120
ttaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tgggccgcac 180
cagccacccc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 240
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 300
agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 360
ggacctatat gggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 420
cctacgacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gaggggaaa 480
tgcagaaaac ttgntatttt ttattattag ccacttgctc gtcttgcttg gtattaagtc 540
gtatttcacn ttgattaatg cnggtggctc cagtgcgcca gattaacttt gtttggatcg 600
aagacgtagt aactggctgg ttatcggaat tgg 633

<210> 35
<211> 569
<212> DNA
<213> E. Coli

<400> 35
tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 60
ttaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tgggccgcac 120
cagccacccg ggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 180
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 240
agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 300
ggacctatat gggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 360
cctacgacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gaggggaaa 420
tgcagaaaac ttttatttt ttattattag ccacttgctc gtcttgcttg ttattagtcg 480
tatttcacgn tgattaatgc ggttgcctcc agtgcgccag atttaacttt gtttgtatcg 540
tagacgtagt aactggctgg tatcggaat 569

<210> 36
<211> 338
<212> DNA
<213> E. Coli

<400> 36
cgtatttaaa tcctttgat tggtgataac atgcgaatcg gtattatttt tccggttgta 60
atcttcatta cagcggtcgt atttttagca tggttttta ttggcggcta tgctgccccg 120
ggagcataaa gatgaaaaaa acaacgatta ttatgatggg tgtggcgatt attgtcgtac 180
tcggcattgc ctgggatggt ggtaacgtca cctctaaaaa atagcaaagg ctgcctgtgt 240
gcagcctttg tgcaatttaa gcgttaactt ttaatcttcc tgtagataaa tagcacgaca 300
atcgcataaa taacggcaac cacgaagctg ccaaaatt 338

<210> 37

<211> 375
<212> DNA
<213> E. Coli

<400> 37
ctgaatattt aaaaaggaaa acgacatgaa accgaagcac agaatcaaca ttctccaatc 60
ataaaatatt tccgtggagc attttattat tgaatataga ggtttaactc cggtaaaaaa 120
caaagaagca ttgaatgcag ggaaaaataa tatggccata aaaaacatcg aaagaaactc 180
ttttaattta acatgtaaac gcatggttaa tcctcatatc acgggtggag tgttaagaac 240
atacataaat ggagtcatgt tttccctttt ccatttatca agttcctgtt gccgttttag 300
tccatctcta attgcatatt ttaatttttc tgataaatgg cattgagcat cgatttcatt 360
taaaacaact gtaca 375

<210> 38
<211> 446
<212> DNA
<213> E. Coli

<400> 38
ttacgatagc tattagtaaa aatataagag ttagctgtat tgttatgtct gtggcgaaat 60
tgactacctt cgtttttttg attaagaatg attttattat cgtaagtaaa attacatgaa 120
tatttaaaaa ggaaaacgac atgaaaccga agcacagaat caacattctc caatcataaa 180
atatttccgt ggagcatttt attattgaat atagaggttt aactccggta aaaaacaaag 240
aagcattgaa tgcagggaaa aataatatgg ccataaaaaa catcgaaaga aactctttta 300
atttaacatg taaacgcatg gttaatcctc atatcacggg tggagtgtta agaacataca 360
taaatggagt catgttttcc cttttccatt tatcaagttc ctgttgccgt tttagtccat 420
ctctaattgc atattttaat ttttct 446

<210> 39
<211> 392
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 39
tcacccggct gccgattttc aggcatcctg atttaactta gcacccgcaa cttaactaca 60
ggaaaacaaa gaaataaatg tctaatcctg atgcaaatcg agccgatttt ttaatcttta 120
cggactttta ccggcctggt ttattaattg cactgtnatc cgggcgttcg cccgctttaa 180
tcacaatagg ctgtgtagcc tgggcctgtt tctctttcac ccgcgccaga gcggcagcaa 240
tcgcatcttt atctttggct gcaggttgaa cggctgcgct cttatgtcgt tcaaggcgag 300
ccgctttttc gcgcttcaga cgagcctggc gcgcttcgaa acgcgctttg gcttctgcgg 360
cncgcttttc ttcctgacga atagccgcaa tt 392

<210> 40
<211> 208
<212> DNA
<213> E. Coli

<400> 40
taataacgct atctgcggat aaagcagaat aggtggttaa ccccagacat aaaccgagga 60
aaataatgtt attgtatttc ataatctatt gttccttagc gacagattgc tgtctgctgg 120
ttcagtaagg taccaggaga aacttcagga agcttgtact cgacaataca gtttgagttt 180
ttatctttgc cccatgaaac ctgtaatt 208

<210> 41
<211> 342
<212> DNA
<213> E. Coli

<400> 41
catcctcaat acegttaaat gcaacccgaa cccccgttgt ccctttgctg cattcactta 60
acgtaatctg aaaagggacg gctggacttg tgctaccggt cgttggaaat tgtctggcac 120
tgtttttttg gagatctacg gtaaaattaa gcgaatccga tgagactgtg cagccataat 180
cgaggangcc cccgctaatt ttaataacgc tatctgcgga taaagcagaa taggtggtta 240
accccagaca taaaccgagg aaaataatgt tattgtattt cataatctat tgttccttag 300
cgacagtttg ctgtctgctg cttcagtaag gtaccaggag aa 342

<210> 42
<211> 841
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(841)
<223> n = A,T,C or G

<400> 42
agatttactg ccaatttccg gcagatcgga aagggttaaa ccatattgat ccataagggt 60
acgaatcacc gctataccgc caggcatggc ttgagccatg gcattaaatt ccgcaaattc 120
gggcgctcat tcttcccacg cggttatttt ggcacacacc agatccagca aggggttntc 180
aggatcgttg agcagcagat gatctaccag ttncagcgcc tgggtgtatt gntccttgtt 240
ctgaataccc gnnagaaaag gtgccacagc anttagcttn tctcctgctt gcaagatgtc 300
tggcaatngc aatcattttt tgcacttant acgatgnaca ncngtaaaga aatcgnattt 360
ttntatnccn tcataacttt acgtatgtan cactttttgc nattcnaaaa aagaccattn 420
gctncaacac gtaaatttna ttgnccccna catttanaac ataaatgntt aaaatttccc 480
ccccncnnan ttttaagntn ttnanagaat ngggaattac ctgcttttna atgnactcan 540
anttttttng naataattcc tntatcnaan ctnnttttcn cccaanagnc nnccaaattn 600
cggtttnntn nttnncnngg cnttttttta cccnanaann tttattcaan nccttttttg 660
tagnctattt naagnggnct ttnttnnatt aactttccnn ttggncaaat tttggcnnat 720
ttttatatan aatntcttta tntcntaatt tnggnanccc cngatgnaan tttatggngg 780
gantcccnnt ccctntttaa tnnatgntct gggntatttt taaancctnn attaannnan 840
c 841

<210> 43
<211> 215
<212> DNA
<213> E. Coli

<400> 43
aataactttt cgttaggcag ttttgggtgt gagttgcaag aggggagact actgaataac 60
tcaagtttta taatcgaggg gaaaatggtg atggcgttca tagcaaaacg ccctcaacca 120
taaaggtcga ggncgcttaa gatgttaaaa acccgctatc cgttaaaaaa caatgttcaa 180
ctaaggtcag tgacattgcg ctaaaaaagc gaatt 215

<210> 44
<211> 395
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(395)
<223> n = A,T,C or G

<400> 44
gcattattca tgagaaatgt gtatcgtaaa tcaactgaaa ttaacgcaac catttgttat 60
ttaaggttta attatctgtg tgtgatattt tattgaatgt tttaaatatt gtttttattg 120
gcattgctat aatattggtt atcatttgct gaatggattc agtcttaatg agtgggtttt 180
taagggatag gcatagagta atgatacgta tgcataacca acatctttac tcattatgtc 240
attgaatgtt gaccctatgt gtttatgaag gagaggtatt ttcagttgat ctggattgnt 300
aaattcatat aatgcgcctt tgctcatgaa tggatgccag tatgtagtgg gaaattataa 360
atattgaaat agtccaacta cttctttatt accaa 395

<210> 45
<211> 843
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(843)
<223> n = A,T,C or G

<400> 45
ataatcaggt aagaaaaggt gcgcggagat taccgtgtgt tgcgatatat tttttagttt 60
cgcgtgtcaa tacatcagtg gcaataaaac gacatatcca gaaaaatata cactaagtga 120
atgatatcct ccgatttatc ttaatcgttt atggataacg gcaaagggct tcgttttttc 180
ctatacttat tcagcactca caaataaagg aacgccaatg aaaattatac tctgggctgt 240
attgattatt ttcctgattg ggctactggt ggtgactggc gtatttaaga tgatatttta 300
aaattaatta atgtcatcag gtccgaaaat aacgagaata tttcagtctc tcatcctgtt 360
gcgctcctgt catgtgcatt gcttcatata atcactggcg caaggagcgc cgcaggcgna 420
gnntgcncgn cgncccacct naccccatgc cgaacttcag aantgaaaac nccntaacnc 480
cgatngtcgg ccggngcctc cccatgcnan agtangggaa ntgccangcg ncnnattaaa 540
cgaaagcctn attncaaaga ctgggccttn cntttatctg atgtttgtcg gagaacgctc 600
tcctgacnan gacaaatncc gccgggagcg gatttgaacn ttgcgaagca accgncccna 660
agggngnngt cntgacnccc nnctctanct nncngccttc ttttgcttna angncctcct 720
ancngatggc ctttttngcc nctctaccaaa cnntttggtt aatgcttnta aaancctttc 780
cannntncaa tccngtnntn cccatccnnn tnntgaaagn ntncctnccn tgtncantnt 840
anntnngggg gnngngngcc ggcggncccc cccccccccc ccc 843

<210> 46
<211> 1024
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(1024)
<223> n = A,T,C or G

<400> 46
gtttatggat aacggcaaag ggcttcgttt tttcctatac ttattcagca ctcacaaata 60
aaggaacgcc aatgaaaatt atactctggg ctgtattgat tattttcctg attgggctac 120
tggtggtgac tggcgtattt aagatgatat tttaaaatta attaatgtca tcaggtccga 180
aaataacgag aatatttcag tctctcatcc tgttgcgctc ctgtcatgtg cattgcttca 240
tataatcact ggcgcaagga gcgcgcagag tnctccnant nnnnntnntt ntntnnctnn 300

nccttcacna tncnnccncn nantnnatag nncaccnntn ttnntcnnnn gnccncctcc 360
nnncnnnnnn ncatnnnatc ccactnnntt tnctccannn nnncnnnntn canccnacaa 420
antncnaccn anntnacctt atacnnannc nancnnnnnn nnccactctn nctcgnnctc 480
cccnttcnac nnccannnnn cancnntcnn ctnnnncccct nncntaattn ttctnnctan 540
ntcctanccn cnnacnnncc cancnatccn nnnatacant cnattnatnn cnntcncntn 600
cnccnnttcc nnctnnncnc tnccncatnc ccnnnannan canntncccc ncctncctna 660
ccncncnnnc ccnccatccc nnnccnncnt ccnnantnga caannnnaat cncnnnnncn 720
nnnnnncnnn tnnncncccn gcncnnccnt nccntcacnc tnnncnncta nannnnntac 780
nntnaccnnt cctnncacnc tnccctnnng antccnacna ntnnnnnanc nanaacnctn 840
tnnnnccata atcccacacc acncccntnc ancntntnnt ncntcntccc ttcntatcnc 900
agctnnnnnt nctntnnnnc tnccncccnn cnnactncnn nnacccncnn cccantcagt 960
ccaccntncn cnncnnnntn nnncnancan ctnncacncn cnantaacct nntnncacct 1020
tccc 1024

<210> 42
<211> 236
<212> DNA
<213> E. Coli

<400> 42
atatacatta agtgaatgat atcttccgat ttatcttaat cgtttatgga taacggcaaa 60
gggcttcttt ttttcctata cttattcagc actcacaaat aaaggaacgc caatgaaaat 120
tatactctgg gctgtattga ttattttcct gattgggcta ctggtggtga ctggcgtatt 180
taagatgata ttttaaaatt aattaatgtc atcaggtccg aaaataacga gaatat 236

<210> 43
<211> 418
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(418)
<223> n = A,T,C or G

<400> 43
cggagattac cgtgtgttgc gatatatttt ttagtttcgc gtggcaatac atcagtggca 60
ataaaacggc atatccagaa aaatatacac taagtgaatg atatcttccg attnatctta 120
ntcgtttatg gataacggca aagggcttcg tttttcctta tacttattca gcactcacaa 180
ataaaggaac gccaatgaaa attatactct gggctgtatt gattattttc ctgattgggc 240
tactggtggt gactggcgta tttaagatga tattttaaaa ttaattaatg tcatcaggtc 300
cgaaaataac gagaatattt cagtctctca tcctgttgcg ctcctgtcat gtgcattgct 360
tcatataatc actggcgcaa ggagcgcgca nggggcggcc aatcgccgcc ggcccctg 418

<210> 44
<211> 550
<212> DNA
<213> E. Coli

<400> 44
ctgctagtta cagggaacac taatgacaga cagctaaaag ccctgtttaa ttacgtatta 60
caaacagggg atgcccagcg ttttcgtgca tttattggtg agatagcgga acgcgcacca 120
caagaaaagg agaaactgat gaccattgct gacagattac gtgaagaagg cgcaatgcag 180
ggcaaacacg aagaagccct gcgtattgct caggagatgc tggatagagg tttagacaga 240
gagttagtta tgatggtgac ccgactttca ccagacgatc ttatcgcgca aagccactaa 300
tcctgtaaca ccgggagtta actggcggat gtttgctgta aaccacatca gcgaacgaca 360
tccgccagcg cctcttctaa atcgtaccag cgaaacgcaa aacccgcttc ttccagccgt 420

ttaggcagcg cgcgttgtcc acctaatacc agtactgaag attcgcccat taacagtcga 480
atggcggtcg cgggacgcg caaaatggcc gggcgatgca gcgcatgacc gagcgcatgg 540
gcaaattgtt 550

<210> 54
<211> 99
<212> DNA
<213> E. Coli

<400> 54
ttggcatcnc ggtgttgccg atcttcatga tatccagccc gccggaaact tcttcccaaa 60
cggttttgct gttatccatt gagtcacgga actgcccct 99

<210> 55
<211> 259
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(259)
<223> n = A,T,C or G

<400> 55
ccgtgcctaa atnatcctgt nacccatcatc cgttgtgaag tagtgattca cgacttcaag 60
gcgcttttca aaaggtatt ttggctttga catattaggg gctattccat ttcatgnccc 120
aacaaaannt gtncagtaca tactcnttgg aaatcaacac aggaggctgg gaatgccgca 180
gaaatatagn ttacttttctt taatagtgat ntgtttcacg cttttatttt tnaaanaagt 240
tnggcttncn tnncgggnn 259

<210> 56
<211> 877
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(877)
<223> n = A,T,C or G

<400> 56
cagcagagcn cggccttctt cgtcagattt cgcagtagtg gtaatggtaa tatccaaacc 60
acgaacgccc tggacttttat cgtagtcgat ttctgggaag atgatctgct cacggacacc 120
catgctgtcg ttacccacgac cgtcgaaaga cttagcggac aggccacgga agtcacggat 180
acgaggtccn gcaatagtga tcaggcgctc aaagaacttc cacatgcgtt cgccacgcag 240
agttacttcn cancgcgatcg gatagccctg acggattttg aagcctgcaa cagatttgcg 300
tgcttttgcn ncncatcgcggtt tttgaccgga gattgctgcc aggtctgctg ctgcgttatc 360
cagcagtttt ttgtcacgca tcgcttcacc aacaccccatg ttcagggtga tcttctcgac 420
ccgagggacn tgcatgacag aattgtagtt aaaacttcagtc atgagttttt taactacttc 480
gtcttttgtcn taatcatgca gtttcgccat cgtactactc catgtcggtg aacgcttccc 540
tgagtagcac aaatccgccg ggagcggatt tgaacgttgc gaagcaacgg cccggagggt 600
ggcgggcagg acgccccgcca taaactgccn ggcatcaaat taagcagaag gccatccctga 660
cggatggcct ttttgcgttt ctacaaactc tttttggttat ttttctaaat catttcaaata 720
tgtatccgnt catccatcc tatcgatgat aagctgtcaa acatgagaat ttaatcaatc 780
taaagttttta tggngttaaa cttgggctgg cagnttncca atggcttaat cagtngaggg 840
ccctatntta acgaactngg ctantttngg tcaatcn 877

<210> 53
<211> 291
<212> DNA
<213> E. Coli

<400> 53
tgaacagcag agatacggcc agtgcggcca atgttttttg tcctttaaac ataacagagt 60
cctttaagga tatagaatag gggtatagct acgccagaat atcgtatttg attattgcta 120
gtttttagtt ttgcttaaaa atattgttag ttttattaaa tgcaaaacta aattattggt 180
atcatgaatt tgttgtatga tgaataaaat ataggggggt atagatagac gtcattttca 240
tagggttata aatgcgacta ccatgaagtt tttaattgaa agtattgggt t 291

<210> 54
<211> 282
<212> DNA
<213> E. Coli

<400> 54
ttattaaatc caaaactaaa ttattggtat catgaatttg ttgtatgatg aataaaatat 60
aggggggtat agatagacgt cattttcata gggttataaa tgcgactacc atgaagtttt 120
taattgaaag tattgggttg ctgataattt gagctgttct atttctttta aatatctata 180
taggtctgtt aatggatttt atttttacaa ttttttgtgt ttaggcatat aaaaatcaac 240
ccgccatatg aacggcgggt taaaatattt acaacttagc aa 282

<210> 55
<211> 293
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(293)
<223> n = A,T,C or G

<400> 55
cggggtcggg cgctcatcaa caatcggggg gcagcaaggg gctgaaacgg gaaagcccct 60
cccgaagaag gggccttgta taaggaaagg gttatgatga agctcgtcat catactggtt 120
gtgtngttac tgttaagttt cccgacttac taacaactca tcagaggggg gagaaatcct 180
cccttatcct tgttccttta ctctaggttg aaaaaacaac agcgtcaata ggcctgccat 240
gtacgaagcc agatctgtga accgctttcc ggttagcctt ttttatcctg ttg 293

<210> 56
<211> 300
<212> DNA
<213> E. Coli

<400> 56
tctgcgttcc gctaaaaggt gcaaatgctc aggacgttgc agcgttttgc gtgaccgctc 60
ggggaagcca aaattgcctc tgggaaagca ttgcgcgggg tccggcgctc atcaacaatc 120
ggggggtagc aacgggctga aacgggaaag cccctcccga agaaggggcc ttgtataagg 180
aaagggttat gatgaagctc gtcatcatac tggttgtgtt gttactgtta agtttcccga 240
cttacttaca aatcatcaga ggggggagaa atcctccctt acccttgttc ctttactcta 300

<210> 57
<211> 309
<212> DNA
<213> E. Coli

<400> 57
caacacagga ggctgggaat gccgcagaaa tatagattac tttctttaat agtgatttgt 60
ttcacgcttt tatttttcac ctggatgata agagattcac tgtgtgaatt gcatattaaa 120
caggagagtt atgagctggc ggcgttttta gcctgcaaat tgaaagagta agagtcttcg 180
gcgggaaatt attcccgcct tacttacggc gttgcgcatt ctcattgcac ccaaatttat 240
tcttcacaaa aataataata gattttatta cgcgatcgat tatttatttc ctgaaaacaa 300
ataaaaaaat ccccgccaaa tggcagggat cttagattct gtgcttttaa gcagagatt 359

<210> 58
<211> 700
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(700)
<223> n = A,T,C or G

<400> 58
aaaccttttt ctcctgtttt tcatagaggg caacccatgt cctgacctgg gttcggggga 60
caccaaaacg tgccgagatg atcctgtaac catcatcagt tgtgaagtag tgattcacga 120
cttcaagggc cttttcaaaa gggtattttg gctttgacat attaggggct attccatttc 180
atcgtccatc aaaatgggtg cagtacatac tcgttggaaa tcaacacagg aggctgggaa 240
tgccgcagaa atatagatta ctttctttaa tagtgatttg tttcacgctt ttatttttca 300
cctggatgat aagagattca ctgtgtgaat tgcatattaa acaggagagt tatgagctgg 360
cggcgttttt agcctgcaaa ttgaaagagt aagagtcttc ggcgggaaat tattcccgcc 420
ttacttacgg cgttgcgcat tctcattgca cccaaattta ttcttcacaa aaataataat 480
agattttatt acgcgatcga ttatttattt cctgaaaaca aataanaaaa tccccgccaa 540
atggcaggga tcttagattc tgtgctttta agcagagatt acaggctggt tacgttacca 600
gctgccggtc ctttaacgcc gctttcgatg gtgaaggaca ctttctgacc ttcgtccaga 660
gattgtaacc atnggtctgg atagccnaga aatgtccaac 700

<210> 59
<211> 631
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G

<400> 59
tggtggcatt ggttgctgga gagagaaaac ccccgcacgt tgcaggtatg cacctgacaa 60
caccacggag gctaatcttg actctagacc actcaagaat agccgcgaaa cgttgtcatt 120
acaacacaag cggctatatg acgttcgcag agctgggcat ggccttctgg catgatttag 180
cggctccggt cattgctggc attcttgcca gtatgatcgt gaactggctg aacaagcgga 240
agtaacgtgt cattgcggcg tcaggctgcc gtaatggcaa tttgcgcccg gaccaggccg 300
caggggcgaa actctgcggc ctttttcgtt cttactgcgg gtaaggcacc cagtcgccgc 360
cgttcagcgg aaggtacggt ttatcctggt attgaataac tactgcattt gagtttctcg 420
agaccggtgc tgtttgtggc aacccactgg tgagtttttt ccagtcaaca ttgtcttcgg 480
tgaaaatctt gcgatcgaga acgcgaacca ccagatcgga gatagccagg aagctgctcg 540
gttgttgcat gacaatcggt gccccctgat gcggtgcctt catgccgaag aatttcaccc 600
caacggcgac gtcngtgata gaccgggcta g 631

<210> 60

<211> 648
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(648)
<223> n = A,T,C or G

<400> 60
ggctcaggcn tgctgattgt ttttttgtgc aatggcccng tattagcgtc gttgctgtcg 60
atggagagaa tcataaacgt ggtgaatgat gattgttagc aaggaaaact gtcaaaaatc 120
ttcaaaaaat ttgagggata aggccggaat ggctccggcc agagggaagt taaccgcgaa 180
gctgttgctg cttgagggtc gttttaacca gacgccaggc gctccatacg ccaaaaccgc 240
gtctggccca gcggaccagc atattaggat ggcgaatcgt ccagatcgcc atcacgctac 300
tgccaaccag ccgccaggag cgcagactta gcagcatatt ccancgacga tcgtaagcgc 360
ctgttgtctc cagccattca cgacgactgg cggaagggnc cgcgnctgac caacttgnct 420
tttagnctca tncanattan attnataaac gcagnanncn ggtntgatta atcntatttn 480
gctccngtct ggtagttagc nncggnnngt ctcnttntna cccnnttcnn tttannttac 540
natnngtaan ttatnttfnt nngtctnant tntanttgng tactntaagt ntatncgnnn 600
atnntnnnan nnnncagnnc ntnttttttta aatnntttnt nannennc 648

<210> 61
<211> 737
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(737)
<223> n = A,T,C or G

<400> 61
tgctaatatc tttctcattg agatgaaaat taaggtaagc gaggaaacac accacaccat 60
aaacggagtc aaataatgct gggtaatatg aatgttttta tggccgtact gggaataatt 120
ttattttctg gtttctggc cgcgtatttc agccacaaat gggatgacta atgaacggag 180
ataatcctcc acctaaccgg ccccttgtta cagttgtgta caaggggcct gatttttatg 240
acggcgaaaa aaaaccgcca gtaaaccggc ggtgaatgct tgcatggata gatttgtgtt 300
ttgctttacc gctaacaggc attttcctgc actgataacg aatcgttgac acagtagcat 360
cagttttctc aatgaatgtt aaacggagct taaactcggt taatcacatt ttgttcgtca 420
ataaacatcc agcgatttct tccggtttgc ttaccctcat acattgcccg gtccgctctt 480
ccaatgacca catccagagg ctcttcagga aatgcgcgac tcacacctgc tgtcacggta 540
atgttgatat gcccttcaga atgtgtgatg gcatggttat cgactaactg gcaaattctg 600
acacctgcac gacatgcttc ttcatcatta gccgctttga caataatgat aaattcttcg 660
ccccgtaccc gataaaccgt ttcgtaatna cgcgtccaac tgggntaagt aaagttgcca 720
gggtgccnta atcttac 737

<210> 62
<211> 648
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(648)
<223> n = A,T,C or G

<400> 62
tgcttttgaa tatgtgctcg caatcttgag aaggaaatgg cgaccacgaa agaaaaggca 60
aaaaccgata atctgaaaga accaagtat ttcagtataa gcattgaatg ccgaccagta 120
aactcttccg gattcaccca gaaagtgaan ccaaaatgat aatcgtatac ataagtcttt 180
cgagtgccta gttagcaaaa agtttcaaca atggagtaaa tacatccaac atatcaataa 240
ctctcaaccg taaggggatt gaaaatggtaa ccccagctct tcgcttgagg ggtatagccg 300
agaccacccga agcccggag gtggtgaaat aaaaccgggc acaacacgaa agggcgcatt 360
tccgatatcn atcaaaagaag tcgggtcttt gtctggtaaa attaaattgg tgggaagtgc 420
gcctccgtcn tgtaaatacc gactttgctg ggtgtagcct ggcggcatca agttttttcc 480
tggaagttcg ctgatgtccg ccctttttaa agggaatttt ggtgatgccg gtcgaatgccg 540
cttaaccccn cgtgggccca gttaaaagtc atggtaagnc ctaatnggtt tgggggtggga 600
aaagccnact gnnaattggt taccctggttt gcaagtancc ctggaagg 648

<210> 63
<211> 237
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(237)
<223> n = A,T,C or G

<400> 63
ggtgtttann tncaagagat tcatctttgt ntaaancccn gataagtaat tacgcataaa 60
acaacaatga ttataatagc aaaaataaat attatcatct ttgatagatt acttgagata 120
gccagcatcn tgtaaagcct ttatcgtttt tttatgctct ggattaatat aatcactaca 180
tctatctnng cnatctgttg ttgatggaca tgtcaaccca tggtcattta cagccaa 237

<210> 64
<211> 427
<212> DNA
<213> E. Coli

<400> 64
gataattaaa gtttgtcgtc agaaaattga cgttacccat aacaaatgaa aggccaggta 60
aatcatncca ttagtcattg ttgctatcgg tgtaatcttg ttgttgcttc tgatgatccg 120
cttcaaaatg aacggcttca tcgcttctgt cttcgtggcg cttgctgttg gattaatgca 180
aggaatncag ctngataaag ttattggctc catcaaagcc ggtgtcgggg ggacgctcgg 240
tagccttgcc ctnatcatgg gttttggcgc aatgctgggc aaaatgctgg cagactgcgg 300
tggcgcaaaa cgnatcgcca ccacgctgat tgccaaattt ggtaaaaaac acatccagtg 360
ggcggtcgta ctnaccggtt ttaccgttgg tttttgcctg ttctatgaag tgggctttgt 420
gctgatg 427

<210> 65
<211> 261
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(261)
<223> n = A,T,C or G

<400> 65
caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatta ttaggaagga 60
aattaatgca attatcgaaa attcaaaaaa tatccaaaaa tngtatactt tattccagaa 120

gagttcaata taatgtttgt cttcaatttt tcttacttca gggtaatata gattgctcat 180
tacattgtga gtttcatctt tatttaattt tctgttgact ccagctctcc gtgataacgg 240
ttttataatt agatgcttat c 261

<210> 66
<211> 96
<212> DNA
<213> E. Coli

<400> 66
agatgattgc cgggaacttg ttagcggcac gcaggcggcg gctcgcaccc ttaccctgct 60
ctttacgtac ttctgcgttg atagtaaaca tttctttc 98

<210> 67
<211> 360
<212> DNA
<213> E. Coli

<400> 67
aagcgcgaaa gaagtcgatg tgctgcagct tcggtttgta cgggtgacgc tgtacgtcct 60
gagctttaaa cttgatttct ttacgtcaaa caacgatggt cagaacttcg ctgtagaatt 120
cagctttagg ttgcatgttc atgactttgt cgtgatccag ctcgatagcc agcggcgctt 180
ctttgctacc gtagatgatt gccgggaact tgttagcggc acgcaggcgg cgggctcgcac 240
cttacgctg ctctttacgt 260

<210> 68
<211> 96
<212> DNA
<213> E. Coli

<400> 68
aaaaacgggcg taaagaaagg ttgcaaacat gttaataaaa actcaaattg atccgacgta 60
tatatttacgc cgcaaaattcc ttacaataaa cagggg 96

<210> 69
<211> 174
<212> DNA
<213> E. Coli

<400> 69
ttaattatta aaatagtgta acgcgattat gtggttatgg gggtaaacat taaataaacc 60
agcgggtaagg ggaaggtaaag tgaaaaaata aaaagcggat aatcttaata agcaggcggg 120
acagcatcgc cattcggcac tgatacgagg tttatttcag ctcatcaacc atcg 174

<210> 70
<211> 138
<212> DNA
<213> E. Coli

<400> 70
agtctgtaaa aaagtcaaaa agagtgtttt atcaacagaa gaatggaggt ctgacagata 60
gtagtaatgt aaaaaaatgg agacttaagt tgaatgaacg ggagtaaagc gaaaagacta 120
tagagtgaa gaaaaatt 138

<210> 71
<211> 101
<212> DNA

<213> E. Coli

<400> 71
tttgttgggt taatattcta ttgttatctt tatttataga tgtttatatt gcatgaggtg 60
gtttttggat agaagaatga ggaagatgcg tcgagccaca gaaacgttag ctttacatat 120
agcggaggtc atgtgaattt aatttacaat agaaataatt tacatatcaa acagttagat 180
gctttttgtc g 191

<210> 72
<211> 244
<212> DNA
<213> E. Coli

<400> 72
ggccatttat acaggaaaag cctatgtcag aacgtaaaaa ctcaaaatca cgccgtaatt 60
atctcgttaa atgttcctgc ccaaactgca cccaagagtc agaacacagt tttcaagag 120
tacaaaaagg tgcccttttg atctgccctc attgcaacaa agtattccag acaaatctta 180
aagctgtagc ctgattgatt ttattagtaa caagtatttt ttatatttta ataatatatt 240
taaa 244

<210> 73
<211> 327
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(327)
<223> n = A,T,C or G

<400> 73
aaatttcaag gtacctgtc accatacttt tttttctgag cattaatgat attttgagct 60
tcttgaaaat ctttaactcc ccacatttgg tggaaagtat tcatattaaa aggaaggntg 120
aataatttgn ctttataaat cgccagtgga gaattagtaa aacgattaaa ttctactaaa 180
tnattaacca naaaaaaatt cccatatata tttatcattg gtatgaaaaa tatgtgcacc 240
atatttatga atntggatac cctnacagtc ctctgtgtac gcatttccac cgatatgatt 300
tcttttctna atcactaaaa cttttt 327

<210> 74
<211> 150
<212> DNA
<213> E. Coli

<400> 74
gcagtgatcg aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga 60
tgactttcgc cggacgtcag gccgccactt cggtgcggtt acgtccggct ttctttgctt 120
tgtaaagccc caaatctgcc gatttcaacc 150

<210> 75
<211> 360
<212> DNA
<213> E. Coli

<400> 75
gaaagtatct tcgttattga catcactgga aaatataact tgctttttcat tattaaactc 60
gaagcgcgta ccctatctgg acaaacattt atcgagctta ccaaattcct gaagaggttt 120
aactacagat aacatttgcg cgtcctttgc agtaatgccc gtcaaatcct tgacgggcat 180

tatttagatt aaattaccag tatttcttcg gagtgaagaa tattaccagg tatatttaac 240
acccacgttc gcggaccagt cttgatctac gtcaccacca ccgaggtagt tagcatcggt 300
ataggcgctg aagttcttgg tgaagctaaa 330

<210> 76
<211> 144
<212> DNA
<213> E. Coli

<400> 76
tgttttttta caacaacgga gcaaaaggtt tgcccttgtg cagctcaggg ttaaccactt 60
taactatgtt gcgtacgacc ggagatgtcg gtttacattt aacaactgcc attgtattac 120
tcctccaact tactcaggcc cgccaacgaa gtccagattc tggccttctt tcagggtgac 180
gtaagcttct ttcc 194

<210> 77
<211> 168
<212> DNA
<213> E. Coli

<400> 77
tcccttttaa tacccagggtg ttaacgactt cgacttcgac ttcaaacagt ttctgcacag 60
cagctttgat ttctgctttg gtcgcgtctt tagcaacttt gagtactatg gtgttggatt 120
tttccatcgt agtagacgct ttttcagaaa cgtgcggtgc acgcagcacc ttcagcagac 180
gttcttta 188

<210> 78
<211> 173
<212> DNA
<213> E. Coli

<400> 78
acaaaggcgt acaaagcctg tgaagccgga aggctccaca gacagtgcta cttgaaggcc 60
ttactgtttt ttcttaggag cgagcacgat gatcatctgg cggccttcga tcttggttgg 120
gaaggatttc accactgcca gttcttgcaa atcgtctttc acgcgattaa gca 173

<210> 79
<211> 272
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(272)
<223> n = A,T,C or G

<400> 79
tggagaaaac ggctgattga taaagcaatc atcgttctag gggcgttaat tgcgctgctg 60
gaactgatcc cgctttctgc ttcaagcttc tgaactggat acggaaacgt aatnagggct 120
aaagaacgca ctactcttag cccttttaaca tttaacgcat tgtcacgaac tcttctgccg 180
ccgttggctg aatggcgacg ggtattggtc gaaaatcttt ttgggtggcc ccatcttttaa 240
cgcccatccc cgaaacctg caacatttcg tc 272

<210> 80
<211> 279
<212> DNA
<213> E. Coli

<400> 80
cgcaggtagc tgatggtcaa caggatgaga gaaacccaga gacaggttaa tcacattgcc 60
tttaaccgct gcacggtaac ctacaccaac cagctgcagc ttcttagtga agccttcggt 120
aacacccata accattgagt tcagcagggc acgcgcggta ccagcctgtg cccaaccgtc 180
tgcgtaacca ttacgcggac cgaaggtcag ggtattatct gcatgtttaa cttcaacagc 240
atcgttgaga gtacgagtc 259

<210> 81
<211> 73
<212> DNA
<213> E. Coli

<400> 81
caggtcggaa cttacccgac aaggaatttc gctaccttag gaccgttata gttacggccg 60
ccgtttaccg gga 73

<210> 82
<211> 666
<212> DNA
<213> E. Coli

<400> 82
atgaacgttt tctcgcaaac tcaacgctat aaggcgttgt tctggttatc gttatttcat 60
ctgctggtga ttacctccag taactatctg gttcagcttc ccgtctccat tttgggtttc 120
catacccacc ggggcgcgtt tagctttccg tttatttttc ttgctaccga cctgaccgtg 180
cgtatttttt gcgcacgcct ggcccgacgc attatcttcg cggtaatgat ccctgcgtta 240
ttaatctcct acctcatctc gtcgctattc tatatgggtt cctggcaggg attcggcgca 300
ctcgccctac ttaacctgtt tgtcgcccgt atcgccaccg ccagtttcat ggcctacgcg 360
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ctggcaccga catcgtccac actgttcggt aacgtcagcg acacgctggc ctttttcttc 480
attgcctcct ggcgtagccc ggatgccttt atggctgaac actggatgga aatcgcgctg 540
gtcgattact gtttcaaagt gttaatcagt atcgttttct tcctgccaat gtatggcgta 600
ttactcaata tgctgttgaa aagactggca gataaatccg aaatcaacgc tttgcaggcg 660
agttaa 666

<210> 83
<211> 612
<212> DNA
<213> E. Coli

<400> 83
gtgataaaat ggatgaatga gccgttatgg ccgtttatcg aaaggaagaa gtcaatgcgc 60
aatctggctt aatatgtcgg aattggcctg ctggttatgg ggcttgcggc ctgtgatgat 120
aaagacaata accctacggc gcagggtcgg gtcgcggaaa gtaacgctac cgggaatccc 180
gtcaaccagc ttcatggcaa gttaagtttc tcgctgccag cggatatgac cgaccagagc 240
ggtaagcagc gaacgcaggc caataacatg catgtctggt ccgacgccac cgggcagaaa 300
gcagtcatcg tcatcatggg cgatgatccg aaagaagatc tggcggtgct ggcgaagcgt 360
ctggaagatc agcaacgtag ccgcgatccg cagctgcaag tggtaaccaa taaagccatt 420
gagctgaaag gtcacaaaat gcagcagtta gacagtatta tctccgcgaa aggccagacg 480
gcgtactctt ctcttattct gggtaacgtg ggtaatcaac tgctgaccat gcaaattacg 540
ctgcccgctg atgatcagca aaaagcgcag accaccgcag aaaacatcat taatacgctg 600
gttattcagt aa 612

<210> 84
<211> 975
<212> DNA

<213> E. Coli

<400> 84

atggcgaata tgtttgccct gattctggtg attgccacac tggtgacggg cattttatgg 60
tgcgtggata aattcttttt cgcacctaaa cggcgggaac gtcaggcagc ggcgcaggcg 120
gctgccgggg actcactgga taaagcaacg ttgaaaaagg ttgcgccgaa gcctggctgg 180
ctggaaaccg gtgcttctgt tttccggta ctggctatcg tattgattgt gcgttcgttt 240
atttatgaac cgttccagat cccgtcaggt tcgatgatgc cgactctgtt aattggtgat 300
tttattctgg tagagaagtt tgcttatggc attaaagatc ctatctacca gaaaacgctg 360
atcgaaaccg gtcatccgaa acgcggcgat atcgtggtct ttaaatatcc ggaagatcca 420
aagcttgatt acatcaagcg cgcggtgggt ttaccgggcg ataaagtcac ttacgatccg 480
gtctcaaaag agctgacgat tcaaccggga tgcagttccg gccaggcgtg tgaaaacgcg 540
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<211> 540
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<213> E. Coli

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<213> E. Coli

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<211> 1029
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<211> 3048
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<212> DNA
<213> E. Coli

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<212> DNA
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<212> DNA
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<211> 1197
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<213> E. Coli

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<211> 291
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<210> 146
<211> 948
<212> DNA
<213> E. Coli

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<211> 891
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<212> DNA
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<211> 117
<212> DNA
<213> E. Coli

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<210> 152
<211> 1632
<212> DNA
<213> E. Coli

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<212> DNA
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<211> 396
<212> DNA
<213> E. Coli

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<211> 405
<212> DNA
<213> E. Coli

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<211> 300
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<213> E. Coli

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<210> 176
<211> 483
<212> DNA
<213> E. Coli

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<210> 177
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<212> DNA
<213> E. Coli

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<211> 612
<212> DNA
<213> E. Coli

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<212> DNA
<213> E. Coli

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<210> 180
<211> 4261
<212> DNA
<213> E. Coli

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<211> 369
<212> DNA
<213> E. Coli

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<211> 711
<212> DNA

<213> E. Coli

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<212> DNA
<213> E. Coli

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<212> DNA
<213> E. Coli

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ggtgaaatta atttacgca ttattttata acaaatattg gagctggatt gcctgatgct 180
tgtgcaagt aa 192

<210> 185
<211> 504
<212> DNA
<213> E. Coli

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<212> DNA
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<213> E. Coli

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<213> E. Coli

<400> 141

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<213> E. Coli

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<211> 93
<212> DNA
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<210> 199
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<211> 597
<212> DNA
<213> E. Coli

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<212> DNA
<213> E. Coli

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<211> 216
<212> DNA
<213> E. Coli

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<212> DNA
<213> E. Coli

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<210> 215
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<213> E. Coli

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<212> DNA
<213> E. Coli

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<213> E. Coli

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<212> DNA
<213> E. Coli

<400> 218
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<210> 219
<211> 1104
<212> DNA
<213> E. Coli

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<213> E. Coli

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<212> DNA
<213> E. Coli

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<212> DNA
<213> E. Coli

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gagtattaa 669

<210> 212
<211> 255
<212> DNA
<213> E. Coli

<400> 212
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<211> 192
<212> DNA
<213> E. Coli

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<212> DNA
<213> E. Coli

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gcagcgaaac tgccgattaa aaccaccttt gtaactaaga cggtgatgta a 411

<210> 226
<211> 702
<212> DNA
<213> E. Coli

<400> 226
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<210> 227
<211> 333
<212> DNA
<213> E. Coli

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<210> 228
<211> 279
<212> DNA
<213> E. Coli

<400> 228
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<210> 229
<211> 822
<212> DNA
<213> E. Coli

<400> 229
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<210> 230
<211> 303
<212> DNA
<213> E. Coli

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<210> 231
<211> 630
<212> DNA
<213> E. Coli

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<211> 606
<212> DNA
<213> E. Coli

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<210> 233
<211> 312
<212> DNA
<213> E. Coli

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<210> 234
<211> 357
<212> DNA
<213> E. Coli

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<212> DNA
<213> E. Coli

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tgcctgccgt acgcataa 198

<210> 236
<211> 543
<212> DNA
<213> E. Coli

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<210> 237

<211> 1929
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<211> 1953
<212> DNA
<213> E. Coli

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<210> 239
<211> 2904
<212> DNA
<213> E. Coli

<400> 239

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agctaccggg cagtgccatt ggcatgacaa cccgaacacc agtgatgcgt ccactccggt      240
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<210> 240
<211> 120
<212> DNA
<213> E. Coli

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<210> 241
<211> 76
<212> DNA
<213> E. Coli

<400> 241
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cccctagggg acgcca 76

<210> 242
<211> 1549
<212> DNA
<213> E. Coli

<400> 242
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aatgtcgcaa gaccaaagag ggggaccttc gggcctcttg ccatcggatg tgcccagatg 240
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<210> 243
<211> 201
<212> PRT
<213> E. Coli

<400> 243

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			20					25					30		
Leu	Pro	Val	Ser	Ile	Leu	Gly	Phe	His	Thr	Thr	Trp	Gly	Ala	Phe	Ser
		35					40					45			
Phe	Pro	Phe	Ile	Phe	Leu	Ala	Thr	Asp	Leu	Thr	Val	Arg	Ile	Phe	Gly
	50					55					60				
Ala	Pro	Leu	Ala	Arg	Arg	Ile	Ile	Phe	Ala	Val	Met	Ile	Pro	Ala	Leu
65					70					75					80
Leu	Ile	Ser	Tyr	Val	Ile	Ser	Ser	Leu	Phe	Tyr	Met	Gly	Ser	Trp	Gln
				85					90					95	
Gly	Phe	Gly	Ala	Leu	Ala	His	Phe	Asn	Leu	Phe	Val	Ala	Arg	Ile	Ala
			100					105					110		
Thr	Ala	Ser	Phe	Met	Ala	Tyr	Ala	Leu	Gly	Gln	Ile	Leu	Asp	Val	His
		115					120					125			
Val	Phe	Asn	Arg	Leu	Arg	Gln	Ser	Arg	Arg	Trp	Trp	Leu	Ala	Pro	Thr
	130					135					140				
Ala	Ser	Thr	Leu	Phe	Gly	Asn	Val	Ser	Asp	Thr	Leu	Ala	Phe	Phe	Phe
145					150					155					160
Ile	Ala	Phe	Trp	Arg	Ser	Pro	Asp	Ala	Phe	Met	Ala	Glu	His	Trp	Met
				165					170					175	
Glu	Ile	Ala	Leu	Val	Asp	Tyr	Cys	Phe	Lys	Val	Leu	Ile	Ser	Ile	Val
			180					185					190		
Phe	Phe	Leu	Pro	Met	Tyr	Gly	Val	Leu	Leu	Asn	Met	Leu	Leu	Lys	Arg
		195					200					205			
Leu	Ala	Asp	Lys	Ser	Glu	Ile	Asn	Ala	Leu	Gln	Ala	Ser			
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<210> 244
<211> 113
<212> PRT
<213> E. Coli

<400> 244

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			20					25					30		
Met	Gly	Leu	Ala	Ala	Cys	Asp	Asp	Lys	Asp	Thr	Asn	Ala	Thr	Ala	Gln
		35					40					45			
Gly	Ser	Val	Ala	Glu	Ser	Asn	Ala	Thr	Gly	Asn	Pro	Val	Asn	Leu	Leu
	50					55					60				
Asp	Gly	Lys	Leu	Ser	Phe	Ser	Leu	Pro	Ala	Asp	Met	Thr	Asp	Gln	Ser

65 70 75 80
Gly Lys Leu Gly Thr Gln Ala Asn Asn Met His Val Trp Ser Asp Ala
85 90 95
Thr Gly Gln Lys Ala Val Ile Val Ile Met Gly Asp Asp Pro Lys Glu
100 105 110
Asp Leu Ala Val Leu Ala Lys Arg Leu Glu Asp Gln Gln Arg Ser Arg
115 120 125
Asp Pro Gln Leu Gln Val Val Thr Asn Lys Ala Ile Glu Leu Lys Gly
130 135 140
His Lys Met Gln Gln Leu Asp Ser Ile Ile Ser Ala Lys Gly Gln Thr
145 150 155 160
Ala Tyr Ser Ser Val Ile Leu Gly Asn Val Gly Asn Gln Leu Leu Thr
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Met Gln Ile Thr Leu Pro Ala Asp Asp Gln Gln Lys Ala Gln Thr Thr
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Ala Glu Asn Ile Ile Asn Thr Leu Val Ile Gln
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<211> 245
<212> DNA
<213> E. Coli

<400> 346
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Glu Arg Gln Ala Ala Ala Gln Ala Ala Ala Gly Asp Ser Leu Asp Lys
35 40 45
Ala Thr Leu Lys Lys Val Ala Pro Lys Pro Gly Trp Leu Gln Thr Gly
50 55 60
Ala Ser Val Phe Pro Val Leu Ala Ile Val Leu Ile Val Arg Ser Phe
65 70 75 80
Ile Tyr Glu Pro Phe Gln Ile Pro Ser Gly Ser Met Met Pro Thr Leu
85 90 95
Leu Ile Gly Asp Phe Ile Leu Val Glu Lys Phe Ala Tyr Gly Ile Lys
100 105 110
Asp Pro Ile Tyr Gln Lys Thr Leu Ile Glu Thr Gly His Pro Lys Arg
115 120 125
Gly Asp Ile Val Val Phe Lys Tyr Pro Gln Asp Pro Lys Leu Asp Tyr
130 135 140
Ile Lys Arg Val Ile Gly Leu Pro Gly Asp Lys Val Thr Tyr Asp Pro
145 150 155 160
Val Ser Lys Glu Leu Thr Ile Gln Pro Gly Cys Ser Ser Gly Gln Ala
165 170 175
Cys Glu Asn Ala Leu Pro Val Thr Tyr Ser Asn Val Glu Pro Ser Asp
180 185 190
Phe Val Gln Thr Phe Ser Arg Arg Asn Gly Gly Glu Ala Thr Ser Gly
195 200 205
Phe Phe Gln Val Pro Lys Asn Gln Thr Lys Gln Asn Gly Ile Arg Leu
210 215 220
Ser Gln Arg Lys Glu Thr Leu Gly Asp Val Thr His Arg Ile Leu Thr
225 230 235 240
Val Pro Ile Ala Gln Asp Gln Val Gly Met Tyr Tyr Gln Gln Pro Gly
245 250 255

Gln Gln Leu Ala Thr Trp Ile Val Pro Pro Gly Gln Tyr Phe Met Met
250 255 260 265 270
Gly Asp Asn Arg Asp Asn Ser Ala Asp Ser Arg Tyr Trp Gly Phe Val
275 280 285
Pro Glu Ala Asn Leu Val Gly Arg Ala Thr Ala Ile Trp Met Ser Phe
290 295 300
Asp Lys Gln Glu Gly Glu Trp Pro Thr Gly Leu Arg Leu Ser Arg Ile
305 310 315 320
Gly Gly Ile His

<210> 246
<211> 344
<212> PRT
<213> E. Coli

<400> 246
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Pro Leu Phe Ser Asp Thr Gln Pro Arg Leu Gln Phe Ala Leu Glu Gln
35 40 45
Leu Leu His Thr Arg Ala Ser Ser Ser Phe Met Leu Ala Lys Ala Pro
50 55 60
Glu Gln Ser Glu Tyr Leu Asn Leu Ile Ala Asn Ala Ala Arg Thr Leu
65 70 75 80
Gln Ser Asp Ala Gly Gln Leu Val Gly Gly His Tyr Glu Val Ser Gly
85 90 95
His Ser Ile Arg Leu Arg His Ala Val Ser Ala Asp Asp Asn Phe Ala
100 105 110
Thr Leu Thr Gln Val Val Ala Ala Asp Trp Val Glu Ala Glu Gln Leu
115 120 125
Phe Gly Cys Leu Arg Gln Phe Asn Gly Asp Ile Thr Leu Gln Pro Gly
130 135 140
Leu Val His Gln Ala Asn Gly Gly Ile Leu Ile Ile Ser Leu Arg Thr
145 150 155 160
Leu Leu Ala Gln Pro Leu Leu Trp Met Arg Leu Lys Asn Ile Val Asn
165 170 175
Arg Glu Arg Phe Asp Trp Val Ala Phe Asp Glu Ser Arg Pro Leu Pro
180 185 190
Val Ser Val Pro Ser Met Pro Leu Lys Leu Lys Val Ile Leu Val Gly
195 200 205
Glu Arg Glu Ser Leu Ala Asp Phe Gln Glu Met Glu Pro Glu Leu Ser
210 215 220
Glu Gln Ala Ile Tyr Ser Glu Phe Glu Asp Thr Leu Gln Ile Val Asp
225 230 235 240
Ala Glu Ser Val Thr Gln Trp Cys Arg Trp Val Thr Phe Thr Ala Arg
245 250 255
His Asn His Leu Pro Ala Pro Gly Ala Asp Ala Trp Pro Ile Leu Ile
260 265 270
Arg Glu Ala Ala Arg Tyr Thr Gly Glu Gln Glu Thr Leu Pro Leu Ser
275 280 285
Pro Gln Trp Ile Leu Arg Gln Cys Lys Glu Val Ala Ser Leu Cys Asp
290 295 300

Gly Asp Thr Phe Ser Gly Glu Gln Leu Asn Leu Met Leu Gln Gln Arg
305 310 315 320
Glu Trp Arg Glu Gly Phe Leu Ala Glu Arg Met Gln Asp Glu Ile Leu
325 330 335
Gln Gln Gln Ile Leu Ile Glu Thr Glu Gly Glu Arg Ile Gly Gln Ile
340 345 350
Asn Ala Leu Ser Val Ile Glu Phe Pro Gly His Pro Arg Ala Phe Gly
355 360 365
Glu Pro Ser Arg Ile Ser Cys Val Val His Ile Gly Asp Gly Glu Phe
370 375 380
Thr Asp Ile Glu Arg Lys Ala Glu Leu Gly Gly Asn Ile His Ala Lys
385 390 395 400
Gly Met Met Ile Met Gln Ala Phe Leu Met Ser Glu Leu Gln Leu Glu
405 410 415
Gln Gln Ile Pro Phe Ser Ala Ser Leu Thr Phe Glu Gln Ser Tyr Ser
420 425 430
Glu Val Asp Gly Asp Ser Ala Ser Met Ala Glu Leu Cys Ala Leu Ile
435 440 445
Ser Ala Leu Ala Asp Val Pro Val Asn Gln Ser Ile Ala Ile Thr Gly
450 455 460
Ser Val Asp Gln Phe Gly Arg Ala Gln Pro Val Gly Gly Leu Asn Glu
465 470 475 480
Lys Ile Glu Gly Phe Phe Ala Ile Cys Gln Gln Arg Glu Leu Thr Gly
485 490 495
Lys Gln Gly Val Ile Ile Pro Thr Ala Asn Val Arg His Leu Ser Leu
500 505 510
His Ser Glu Leu Val Lys Ala Val Glu Glu Gly Lys Phe Thr Ile Trp
515 520 525
Ala Val Asp Asp Val Thr Asp Ala Leu Pro Leu Leu Leu Asn Leu Val
530 535 540
Trp Asp Gly Glu Gly Gln Thr Thr Leu Met Gln Thr Ile Gln Glu Arg
545 550 555 560
Ile Ala Gln Ala Ser Gln Gln Glu Gly Arg His Arg Phe Pro Trp Pro
565 570 575
Leu Arg Trp Leu Asn Trp Phe Ile Pro Asn
580 585

<210> 147
<211> 394
<212> PRT
<213> E. Coli

<400> 147
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35 40 45
Gln Ile Asp Asn Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
50 55 60
Thr Ser His Val Glu Tyr Asp Thr Pro Thr Arg His Tyr Ala His Val
65 70 75 80
Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
85 90 95
Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro

100 105 110
Met Pro Gln Thr Arg Glu His Ile Leu Leu Gly Arg Gln Val Gly Val
115 120 125
Pro Tyr Ile Ile Val Phe Leu Asn Lys Cys Asp Met Val Asp Asp Glu
130 135 140
Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ser Gln
145 150 155 160
Tyr Asp Phe Pro Gly Asp Asp Thr Pro Ile Val Arg Gly Ser Ala Leu
165 170 175
Lys Ala Leu Glu Gly Asp Ala Glu Trp Glu Ala Lys Ile Leu Glu Leu
180 185 190
Ala Gly Phe Leu Asp Ser Tyr Ile Pro Glu Pro Glu Arg Ala Ile Asp
195 200 205
Lys Pro Phe Leu Leu Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg
210 215 220
Gly Thr Val Val Thr Gly Arg Val Glu Arg Gly Ile Ile Lys Val Gly
225 230 235 240
Glu Glu Val Glu Ile Val Gly Ile Lys Glu Thr Gln Lys Ser Thr Cys
245 250 255
Thr Gly Val Glu Met Phe Arg Lys Leu Leu Asp Glu Gly Arg Ala Gly
260 265 270
Glu Asn Val Gly Val Leu Leu Arg Gly Ile Lys Arg Glu Glu Ile Glu
275 280 285
Arg Gly Gln Val Leu Ala Lys Pro Gly Thr Ile Lys Pro His Thr Lys
290 295 300
Phe Glu Ser Glu Val Tyr Ile Leu Ser Lys Asp Glu Gly Gly Arg His
305 310 315 320
Thr Pro Phe Phe Lys Gly Tyr Arg Pro Gln Phe Tyr Phe Arg Thr Thr
325 330 335
Asp Val Thr Gly Thr Ile Glu Leu Pro Glu Gly Val Glu Met Val Met
340 345 350
Pro Gly Asp Asn Ile Lys Met Val Val Thr Leu Ile His Pro Ile Ala
355 360 365
Met Asp Asp Gly Leu Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Val
370 375 380
Gly Ala Gly Val Val Ala Lys Val Leu Gly
385 390

<210> 34
<211> 704
<212> PRT
<213> E. Coli

<400> 34
Met Ala Arg Thr Thr Pro Ile Ala Arg Tyr Arg Asn Ile Gly Ile Ser
1 5 10 15
Ala His Ile Asp Ala Gly Lys Thr Thr Thr Thr Glu Arg Ile Leu Phe
20 25 30
Tyr Thr Gly Val Asn His Lys Ile Gly Glu Val His Asp Gly Ala Ala
35 40 45
Thr Met Asp Trp Met Glu Gln Glu Gln Glu Arg Gly Ile Thr Ile Thr
50 55 60
Ser Ala Ala Thr Thr Ala Phe Trp Ser Gly Met Ala Lys Gln Tyr Glu
65 70 75 80
Pro His Arg Ile Asn Ile Ile Asp Thr Pro Gly His Val Asp Phe Thr

```
                    85                  90                  95
Ile Glu Val Glu Arg Ser Met Arg Val Leu Asp Gly Ala Val Met Val
            100                 105                 110
Tyr Cys Ala Val Gly Gly Val Gln Pro Gln Ser Glu Thr Val Trp Arg
        115                 120                 125
Gln Ala Asn Lys Tyr Lys Val Pro Arg Ile Ala Phe Val Asn Lys Met
    130                 135                 140
Asp Arg Met Gly Ala Asn Phe Leu Lys Val Val Asn Gln Ile Lys Thr
145                 150                 155                 160
Arg Leu Gly Ala Asn Pro Val Pro Leu Gln Leu Ala Ile Gly Ala Glu
                165                 170                 175
Glu His Phe Thr Gly Val Val Asp Leu Val Lys Met Lys Ala Ile Asn
            180                 185                 190
Trp Asn Asp Ala Asp Gln Gly Val Thr Phe Glu Tyr Glu Asp Ile Pro
        195                 200                 205
Ala Asp Met Val Glu Leu Ala Glu Glu Trp His Glu Asn Leu Ile Glu
    210                 215                 220
Ser Ala Ala Glu Ala Ser Glu Glu Leu Met Glu Lys Tyr Leu Gly Gly
225                 230                 235                 240
Glu Glu Leu Thr Glu Ala Glu Ile Lys Gly Ala Leu Arg Gln Arg Val
                245                 250                 255
Leu Asn Asn Gln Ile Ile Leu Val Thr Cys Gly Ser Ala Phe Lys Asn
            260                 265                 270
Lys Gly Val Gln Ala Met Leu Asp Ala Val Ile Asp Tyr Leu Pro Ser
        275                 280                 285
Pro Val Asp Val Pro Ala Ile Asn Gly Ile Leu Asp Asp Gly Lys Asp
    290                 295                 300
Thr Pro Ala Glu Arg His Ala Ser Asp Asp Glu Pro Phe Ser Ala Leu
305                 310                 315                 320
Ala Phe Lys Ile Ala Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe
                325                 330                 335
Arg Val Tyr Ser Gly Val Val Asn Ser Gly Asp Thr Val Leu Asn Ser
            340                 345                 350
Val Lys Ala Ala Arg Glu Arg Phe Gly Arg Ile Val Gln Met His Ala
        355                 360                 365
Asn Lys Arg Glu Glu Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala
    370                 375                 380
Ala Ile Gly Leu Lys Asp Val Thr Thr Gly Asp Thr Leu Cys Asp Pro
385                 390                 395                 400
Asp Ala Pro Ile Ile Leu Glu Arg Met Glu Phe Pro Glu Pro Val Ile
                405                 410                 415
Ser Ile Ala Val Glu Pro Lys Thr Lys Ala Asp Gln Glu Lys Met Gly
            420                 425                 430
Leu Ala Leu Gly Arg Leu Ala Lys Glu Asp Pro Ser Phe Arg Val Trp
        435                 440                 445
Thr Asp Glu Glu Ser Asn Gln Thr Ile Ile Ala Gly Met Gly Glu Leu
    450                 455                 460
His Leu Asp Ile Ile Val Asp Arg Met Lys Arg Glu Phe Asn Val Glu
465                 470                 475                 480
Ala Asn Val Gly Lys Pro Gln Val Ala Tyr Arg Glu Thr Ile Arg Gln
                485                 490                 495
Lys Val Thr Asp Val Glu Gly Lys His Ala Lys Gln Ser Gly Gly Arg
            500                 505                 510
Gly Gln Tyr Gly His Val Val Ile Asp Met Tyr Pro Leu Gln Pro Gly
        515                 520                 525
Ser Asn Pro Lys Gly Tyr Glu Phe Ile Asn Asp Ile Lys Gly Gly Val
    530                 535                 540
```

Ile Pro Gly Glu Tyr Ile Pro Ala Val Asp Lys Gly Ile Gln Glu Gln
545 550 555 560
Leu Lys Ala Gly Pro Leu Ala Gly Tyr Pro Val Val Asp Met Gly Ile
565 570 575
Arg Leu His Phe Gly Ser Tyr His Asp Val Asp Ser Ser Glu Leu Ala
580 585 590
Phe Lys Leu Ala Ala Ser Ile Ala Phe Lys Glu Gly Phe Lys Lys Ala
595 600 605
Lys Pro Val Leu Leu Glu Pro Ile Met Lys Val Glu Val Glu Thr Pro
610 615 620
Glu Glu Asn Thr Gly Asp Val Ile Gly Asp Leu Ser Arg Arg Arg Gly
625 630 635 640
Met Leu Lys Gly Gln Glu Ser Glu Val Thr Gly Val Lys Ile His Ala
645 650 655
Glu Val Pro Leu Ser Glu Met Phe Gly Tyr Ala Thr Gln Leu Arg Ser
660 665 670
Leu Thr Lys Gly Arg Ala Ser Tyr Thr Met Glu Phe Leu Lys Tyr Asp
675 680 685
Glu Ala Pro Ser Asn Val Ala Gln Ala Val Ile Glu Ala Arg Gly Lys
690 695 700

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: E. Coli

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Pro Asn Arg Arg Val Ile Gly Gln Arg Lys Ile Leu Pro Asp Pro
1 5 10 15
Lys Phe Gly Ser Glu Leu Leu Ala Lys Phe Val Asn Ile Leu Met Val
20 25 30
Asp Gly Lys Lys Ser Thr Ala Glu Ser Ile Val Tyr Ser Ala Leu Glu
35 40 45
Thr Leu Ala Gln Arg Ser Gly Lys Ser Glu Leu Glu Ala Phe Glu Val
50 55 60
Ala Leu Glu Asn Val Arg Pro Thr Val Glu Val Lys Ser Arg Arg Val
65 70 75 80
Gly Gly Ser Thr Tyr Gln Val Pro Val Glu Val Arg Pro Val Arg Arg
85 90 95
Asn Ala Leu Ala Met Arg Trp Ile Val Glu Ala Ala Arg Lys Arg Gly
100 105 110
Asp Lys Ser Met Ala Leu Arg Leu Ala Asn Glu Leu Ser Asp Ala Ala
115 120 125
Glu Asn Lys Gly Thr Ala Val Lys Lys Arg Glu Asp Val His Arg Met
130 135 140
Ala Glu Ala Asn Lys Ala Phe Ala His Tyr Arg Trp Leu Ser Leu Arg
145 150 155 160
Ser Phe Ser His Gln Ala Gly Ala Ser Ser Lys Gln Pro Ala Leu Gly
165 170 175
Tyr Leu Asn

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(213) E. Coli

(400) 250

Met Ala Thr Val Asn Gln Leu Val Arg Lys Pro Arg Ala Arg Lys Val
1 5 10 15
Ala Lys Ser Asn Val Pro Ala Leu Glu Ala Cys Pro Gln Lys Arg Gly
20 25 30
Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala
35 40 45
Leu Arg Lys Val Cys Arg Val Arg Leu Thr Asn Gly Phe Glu Val Thr
50 55 60
Ser Tyr Ile Gly Gly Glu Gly His Asn Leu Gln Glu His Ser Val Ile
65 70 75 80
Leu Ile Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr His
85 90 95
Thr Val Arg Gly Ala Leu Asp Cys Ser Gly Val Lys Asp Arg Lys Gln
100 105 110
Ala Arg Ser Lys Tyr Gly Val Lys Arg Pro Lys Ala
115 120

(211) 251
(211) 165
(212) PRT
(213) E. Coli

(400) 251

Met Ala Leu Asn Leu Gln Asp Lys Gln Ala Ile Val Ala Glu Val Ser
1 5 10 15
Glu Val Ala Lys Gly Ala Leu Ser Ala Val Val Ala Asp Ser Arg Gly
20 25 30
Val Thr Val Asp Lys Met Thr Glu Leu Arg Lys Ala Gly Arg Glu Ala
35 40 45
Gly Val Tyr Met Arg Val Val Arg Asn Thr Leu Leu Arg Arg Ala Val
50 55 60
Glu Gly Thr Pro Phe Glu Cys Leu Lys Asp Ala Phe Val Gly Pro Thr
65 70 75 80
Leu Ile Ala Tyr Ser Met Glu His Pro Gly Ala Ala Ala Arg Leu Phe
85 90 95
Lys Glu Phe Ala Lys Ala Asn Ala Lys Phe Glu Val Lys Ala Ala Ala
100 105 110
Phe Glu Gly Glu Leu Ile Pro Ala Ser Gln Ile Asp Arg Leu Ala Thr
115 120 125
Leu Pro Thr Tyr Glu Glu Ala Ile Ala Arg Leu Met Ala Thr Met Lys
130 135 140
Glu Ala Ser Ala Gly Lys Leu Val Arg Thr Leu Ala Ala Val Arg Asp
145 150 155 160
Ala Lys Glu Ala Ala
165

(210) 252
(211) 121
(212) PRT
(213) E. Coli

(400) 252

Met Ser Ile Thr Lys Asp Gln Ile Ile Glu Ala Val Ala Ala Met Ser
1 5 10 15
Val Met Asp Val Val Glu Leu Ile Ser Ala Met Glu Glu Lys Phe Gly
20 25 30
Val Ser Ala Ala Ala Ala Val Ala Val Ala Ala Gly Pro Val Glu Ala
35 40 45
Ala Glu Glu Lys Thr Glu Phe Asp Val Ile Leu Lys Ala Ala Gly Ala
50 55 60
Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly Leu Gly
65 70 75 80
Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Ala Leu Lys
85 90 95
Glu Gly Val Ser Lys Asp Asp Ala Glu Ala Leu Lys Lys Ala Leu Glu
100 105 110
Glu Ala Gly Ala Glu Val Glu Val Lys
115 120

<210> 213
<211> 714
<212> PRT
<213> E. Coli

<400> 213
Met Ser Arg Ile Ile Met Leu Ile Pro Thr Gly Thr Ser Val Gly Leu
1 5 10 15
Thr Ser Val Ser Leu Gly Val Ile Arg Ala Met Glu Arg Lys Gly Val
20 25 30
Arg Leu Ser Val Phe Lys Pro Ile Ala Gln Pro Arg Thr Gly Gly Asp
35 40 45
Ala Pro Asp Gln Thr Thr Thr Ile Val Arg Ala Asn Ser Ser Thr Thr
50 55 60
Thr Ala Ala Glu Pro Leu Lys Met Ser Tyr Val Glu Gly Leu Leu Ser
65 70 75 80
Ser Asn Gln Lys Asp Val Leu Met Glu Glu Ile Val Ala Asn Tyr His
85 90 95
Ala Asn Thr Lys Asp Ala Glu Val Val Leu Val Glu Gly Leu Val Pro
100 105 110
Thr Arg Lys His Gln Phe Ala Gln Ser Leu Asn Tyr Glu Ile Ala Lys
115 120 125
Thr Leu Asn Ala Glu Ile Val Phe Val Met Ser Gln Gly Thr Asp Thr
130 135 140
Pro Glu Gln Leu Lys Glu Arg Ile Glu Leu Thr Arg Asn Ser Phe Gly
145 150 155 160
Gly Ala Lys Asn Thr Asn Ile Thr Gly Val Ile Val Asn Lys Leu Asn
165 170 175
Ala Pro Val Asp Glu Gln Gly Arg Thr Arg Pro Asp Leu Ser Glu Ile
180 185 190
Phe Asp Asp Ser Ser Lys Ala Lys Val Asn Asn Val Asp Pro Ala Lys
195 200 205
Leu Gln Gln Ser Ser Pro Leu Pro Val Leu Gly Ala Val Pro Trp Ser
210 215 220
Phe Asp Leu Ile Ala Thr Arg Ala Ile Asp Met Ala Arg His Leu Asn
225 230 235 240
Ala Thr Ile Ile Asn Glu Gly Asp Ile Asn Thr Arg Arg Val Lys Ser
245 250 255
Val Thr Phe Cys Ala Arg Ser Ile Pro His Met Leu Glu His Phe Arg

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                 260                                 265                                 270
Ala Gly Ser Leu Leu Val Thr Ser Ala Asp Arg Pro Asp Val Leu Val
            275                 280                 285
Ala Ala Cys Leu Ala Ala Met Asn Gly Val Glu Ile Gly Ala Leu Leu
        290                 295                 300
Leu Thr Gly Gly Tyr Glu Met Asp Ala Arg Ile Ser Lys Leu Cys Glu
305                 310                 315                 320
Arg Ala Phe Ala Thr Gly Leu Pro Val Phe Met Val Asn Thr Asn Thr
                325                 330                 335
Trp Gln Thr Ser Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val
            340                 345                 350
Asp Asp His Glu Arg Ile Glu Lys Val Gln Glu Tyr Val Ala Asn Tyr
        355                 360                 365
Ile Asn Ala Asp Trp Ile Glu Ser Leu Thr Ala Thr Ser Glu Arg Ser
    370                 375                 380
Arg Arg Leu Ser Pro Pro Ala Phe Arg Tyr Gln Leu Thr Glu Leu Ala
385                 390                 395                 400
Arg Lys Ala Gly Lys Arg Ile Val Leu Pro Glu Gly Asp Glu Pro Arg
                405                 410                 415
Thr Val Lys Ala Ala Ala Ile Cys Ala Glu Arg Gly Ile Ala Thr Cys
            420                 425                 430
Val Leu Leu Gly Asn Pro Ala Glu Ile Asn Arg Val Ala Ala Ser Gln
        435                 440                 445
Gly Val Glu Leu Gly Ala Gly Ile Glu Ile Val Asp Pro Glu Val Val
    450                 455                 460
Arg Glu Ser Tyr Val Gly Arg Leu Val Glu Leu Asn Lys Asn Lys Gly
465                 470                 475                 480
Met Thr Glu Thr Val Ala Arg Glu Gln Leu Glu Asp Asn Val Val Leu
                485                 490                 495
Gly Thr Leu Met Leu Glu Gln Asp Glu Val Asp Gly Leu Val Ser Gly
            500                 505                 510
Ala Val His Thr Thr Ala Asn Thr Ile Arg Pro Pro Leu Gln Leu Ile
        515                 520                 525
Lys Thr Ala Pro Gly Ser Ser Leu Val Ser Ser Val Phe Phe Met Leu
    530                 535                 540
Leu Pro Glu Glu Val Tyr Val Tyr Gly Asp Cys Ala Ile Asn Pro Asp
545                 550                 555                 560
Pro Thr Ala Glu Gln Leu Ala Glu Ile Ala Ile Gln Ser Ala Asp Ser
                565                 570                 575
Ala Ala Ala Phe Gly Ile Glu Pro Arg Val Ala Met Leu Ser Tyr Ser
            580                 585                 590
Thr Gly Thr Ser Gly Ala Gly Ser Asp Val Glu Lys Val Arg Glu Ala
        595                 600                 605
Thr Arg Leu Ala Gln Glu Lys Arg Pro Asp Leu Met Ile Asp Gly Pro
    610                 615                 620
Leu Gln Tyr Asp Ala Ala Val Met Ala Asp Val Ala Lys Ser Lys Ala
625                 630                 635                 640
Pro Asn Ser Pro Val Ala Gly Arg Ala Thr Val Phe Ile Phe Pro Asp
                645                 650                 655
Leu Asn Thr Gly Asn Thr Thr Tyr Lys Ala Val Gln Arg Ser Ala Asp
            660                 665                 670
Leu Ile Ser Ile Gly Pro Met Leu Gln Gly Met Asn Lys Pro Val Asn
        675                 680                 685
Asp Leu Ser Arg Gly Ala Leu Val Asp Asp Ile Val Tyr Thr Ile Ala
    690                 695                 700
Leu Thr Ala Ile Gln Ser Ala Gln Gln Gln
705                 710
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<210> 254
<211> 388
<212> PRT
<213> E. Coli

<400> 254

Met Asn Asn Ser Ile Asn His Lys Phe His His Ile Ser Arg Ala Glu
1 5 10 15
Tyr Gln Gln Leu Leu Ala Val Ser Arg Gly Asp Ala Val Ala Asp Tyr
20 25 30
Ile Ile Asp Asn Val Ser Ile Leu Asp Leu Ile Asn Gly Gly Glu Ile
35 40 45
Ser Gly Pro Ile Val Ile Lys Gly Arg Tyr Ile Ala Gly Val Gly Ala
50 55 60
Glu Tyr Thr Asp Ala Pro Ala Leu Gln Arg Ile Asp Ala Arg Gly Ala
65 70 75 80
Thr Ala Val Pro Gly Phe Ile Asp Ala His Leu His Ile Glu Ser Ser
85 90 95
Met Met Thr Pro Val Thr Phe Glu Thr Ala Thr Leu Pro Arg Gly Leu
100 105 110
Thr Thr Val Ile Cys Asp Pro His Glu Ile Val Asn Val Met Gly Glu
115 120 125
Ala Gly Phe Ala Trp Phe Ala Asn Cys Ala Glu Gln Ala Arg Gln Asn
130 135 140
Gln Tyr Leu Gln Val Ser Ser Cys Val Pro Ala Leu Glu Gly Cys Asp
145 150 155 160
Val Asn Gly Ala Ser Phe Thr Leu Glu Gln Met Leu Ala Trp Arg Asp
165 170 175
His Pro Gln Val Thr Gly Leu Ala Glu Met Met Asp Tyr Pro Gly Val
180 185 190
Ile Ser Gly Gln Asn Ala Leu Leu Asp Lys Leu Asp Ala Phe Arg His
195 200 205
Leu Thr Leu Asp Gly His Cys Pro Gly Leu Gly Gly Lys Glu Leu Asn
210 215 220
Ala Tyr Ile Thr Ala Gly Ile Gln Asn Cys His Glu Ser Tyr Gln Leu
225 230 235 240
Glu Glu Gly Arg Arg Lys Leu Gln Leu Gly Met Ser Leu Met Ile Arg
245 250 255
Glu Gly Ser Ala Ala Arg Asn Leu Asn Ala Leu Ala Pro Leu Ile Asn
260 265 270
Glu Phe Asn Ser Pro Gln Cys Met Leu Cys Thr Asp Asp Arg Asn Pro
275 280 285
Trp Glu Ile Ala His Glu Gly His Ile Asp Ala Leu Ile Arg Arg Leu
290 295 300
Ile Glu Gln His Asn Val Pro Leu His Val Ala Tyr Arg Val Ala Ser
305 310 315 320
Trp Ser Thr Ala Arg His Phe Gly Leu Asn His Leu Gly Leu Leu Ala
325 330 335
Pro Gly Lys Gln Ala Asp Ile Val Leu Leu Ser Asp Ala Arg Lys Val
340 345 350
Thr Val Gln Gln Val Leu Val Lys Gly Glu Pro Ile Asp Ala Gln Thr
355 360 365
Leu Gln Ala Glu Glu Ser Ala Arg Leu Ala Gln Ser Ala Pro Pro Tyr
370 375 380
Gly Asn Thr Ile Ala Arg Gln Pro Val Ser Ala Ser Asp Phe Ala Leu

385 390 395 400

Gln Phe Thr Pro Gly Lys Arg Tyr Arg Val Ile Asp Val Ile His Asn
405 410 415

Glu Leu Ile Thr His Ser His Ser Ser Val Tyr Ser Glu Asn Gly Phe
420 425 430

Asp Arg Asp Asp Val Ser Phe Ile Ala Val Leu Glu Arg Tyr Gly Gln
435 440 445

Arg Leu Ala Pro Ala Cys Gly Leu Leu Gly Gly Phe Gly Leu Asn Glu
450 455 460

Gly Ala Leu Ala Ala Thr Val Ser His Asp Ser His Asn Ile Val Val
465 470 475 480

Ile Gly Arg Ser Ala Glu Glu Met Ala Leu Ala Val Asn Gln Val Ile
485 490 495

Gln Asp Gly Gly Gly Leu Cys Val Val Arg Asn Gly Gln Val Gln Ser
500 505 510

His Leu Pro Leu Pro Ile Ala Gly Leu Met Ser Thr Asp Thr Ala Gln
515 520 525

Ser Leu Ala Glu Gln Ile Asp Ala Leu Lys Ala Ala Ala Arg Glu Cys
530 535 540

Gly Pro Leu Pro Asp Glu Pro Phe Ile Gln Met Ala Phe Leu Ser Leu
545 550 555 560

Pro Val Ile Pro Ala Leu Lys Leu Thr Ser Gln Gly Leu Phe Asp Gly
565 570 575

Glu Lys Pro Ala Phe Thr Thr Leu Glu Val Thr Glu
580 585

<210> 133
<211> 409
<212> PRT
<213> E. Coli

<400> 133

Met Ala Tyr Cys Asn Pro Gly Leu Glu Ser Arg Pro Asn Lys Arg Asn
1 5 10 15

Ala Leu Arg Arg His Val Val Thr Gly Ile Gly Met Lys Ile Val Ile
20 25 30

Ala Pro Asp Ser Tyr Lys Glu Ser Leu Ser Ala Ser Glu Val Ala Gln
35 40 45

Ala Ile Glu Lys Gly Phe Arg Glu Ile Phe Pro Asp Ala Gln Tyr Val
50 55 60

Ser Val Pro Val Ala Asp Gly Gly Glu Gly Thr Val Glu Ala Met Ile
65 70 75 80

Ala Ala Thr Gln Gly Ala Glu Arg His Ala Trp Val Thr Gly Pro Leu
85 90 95

Gly Glu Lys Val Asn Ala Ser Trp Gly Ile Ser Gly Asp Gly Lys Thr
100 105 110

Ala Phe Ile Glu Met Ala Ala Ala Ser Gly Leu Gln Leu Val Pro Ala
115 120 125

Glu Lys Arg Asp Pro Leu Val Thr Thr Ser Arg Gly Thr Gly Glu Leu
130 135 140

Ile Leu Gln Ala Leu Glu Ser Gly Ala Thr Asn Ile Ile Ile Gly Ile
145 150 155 160

Gly Gly Ser Ala Thr Asn Asp Gly Gly Ala Gly Met Val Gln Ala Leu
165 170 175

Gly Ala Lys Leu Cys Asp Ala Asn Gly Asn Glu Ile Gly Phe Gly Gly
180 185 190

Gly Ser Leu Asn Thr Leu Asn Asp Ile Asp Ile Ser Gly Leu Asp Pro
195 200 205
Arg Leu Lys Asp Cys Val Ile Arg Val Ala Cys Asp Val Thr Asn Pro
210 215 220
Leu Val Gly Asp Asn Gly Ala Ser Arg Ile Phe Gly Pro Gln Lys Gly
225 230 235 240
Ala Ser Glu Ala Met Ile Val Glu Leu Asp Asn Asn Leu Ser His Tyr
245 250 255
Ala Glu Val Ile Lys Lys Ala Leu His Val Asp Val Lys Asp Val Pro
260 265 270
Gly Ala Gly Ala Ala Gly Gly Met Gly Ala Ala Leu Met Ala Phe Leu
275 280 285
Gly Ala Gln Leu Lys Ser Gly Ile Glu Ile Val Thr Thr Ala Leu Asn
290 295 300
Leu Glu Glu His Ile His Asp Lys Thr Leu Val Ile Thr Gly Glu Gly
305 310 315 320
Arg Ile Asp Ser Gln Ser Ile His Gly Lys Val Pro Ile Gly Val Ala
325 330 335
Asn Val Ala Lys Lys Tyr His Lys Pro Val Ile Gly Ile Ala Gly Ser
340 345 350
Leu Thr Asp Asp Val Gly Val Val His Gln His Gly Ile Asp Ala Val
355 360 365
Phe Ser Val Leu Thr Ser Ile Gly Thr Leu Asp Glu Ala Phe Arg Gly
370 375 380
Ala Tyr Asp Asn Ile Cys Arg Ala Ser Arg Asn Ile Ala Ala Thr Leu
385 390 395 400
Ala Ile Gly Met Arg Asn Ala Gly

<400> 166
Met Ile Asp Met Thr Met Lys Val Gly Phe Ile Gly Leu Gly Ile Met
1 5 10 15
Gly Lys Pro Met Ser Lys Asn Leu Leu Lys Ala Gly Tyr Ser Leu Val
20 25 30
Val Ala Asp Arg Asn Pro Glu Ala Ile Ala Asp Val Ile Ala Ala Gly
35 40 45
Ala Glu Thr Ala Ser Thr Ala Lys Ala Ile Ala Glu Gln Cys Asp Val
50 55 60
Ile Ile Thr Met Leu Pro Asn Ser Pro His Val Lys Glu Val Ala Leu
65 70 75 80
Gly Glu Asn Gly Ile Ile Glu Gly Ala Lys Pro Gly Thr Val Leu Ile
85 90 95
Asp Met Ser Ser Ile Ala Pro Leu Ala Ser Arg Glu Ile Ser Glu Ala
100 105 110
Leu Lys Ala Lys Gly Ile Asp Met Leu Asp Ala Pro Val Ser Gly Gly
115 120 125
Glu Pro Lys Ala Ile Asp Gly Thr Leu Ser Val Met Val Gly Gly Asp
130 135 140
Lys Ala Ile Phe Asp Lys Tyr Tyr Asp Leu Met Lys Ala Met Ala Gly
145 150 155 160
Ser Val Val His Thr Gly Glu Ile Gly Ala Gly Asn Val Thr Lys Leu

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                                165                 170                 175
Ala Asn Gln Val Ile Val Ala Leu Asn Ile Ala Ala Met Ser Glu Ala
            180                 185                 190
Leu Thr Leu Ala Thr Lys Ala Gly Val Asn Pro Asp Leu Val Tyr Gln
        195                 200                 205
Ala Ile Asn Gly Gly Leu Ala Gly Ser Thr Val Leu Asp Ala Lys Ala
    210                 215                 220
Pro Met Val Met Asp Arg Asn Phe Lys Pro Gly Phe Arg Ile Asp Leu
225                 230                 235                 240
His Ile Lys Asp Leu Ala Asn Ala Leu Asp Thr Ser His Gly Val Gly
                245                 250                 255
Ala Gln Leu Pro Leu Thr Ala Ala Val Met Glu Met Met Gln Ala Leu
            260                 265                 270
Arg Ala Asp Gly Leu Gly Thr Ala Asp His Ser Ala Leu Ala Cys Tyr
        275                 280                 285
Tyr Glu Lys Leu Ala Lys Val Glu Val Thr Arg
    290                 295
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<211> 1317
<212> DNA
<213> PRT
<213> E. Coli

<400> 187

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Met Asn Asn Asp Val Phe Pro Asn Lys Phe Lys Ala Ala Leu Ala Ala
 1               5                  10                  15
Lys Gln Val Gln Ile Gly Cys Trp Ser Ala Leu Ser Asn Pro Ile Ser
            20                  25                  30
Thr Glu Val Leu Gly Leu Ala Gly Phe Asp Trp Leu Val Leu Asp Gly
        35                  40                  45
Glu His Ala Pro Asn Asp Ile Ser Thr Phe Ile Pro Gln Leu Met Ala
    50                  55                  60
Leu Lys Gly Ser Ala Ser Ala Pro Val Val Arg Val Pro Thr Asn Glu
65                  70                  75                  80
Pro Val Ile Ile Lys Arg Leu Leu Asp Ile Gly Phe Tyr Asn Phe Leu
                85                  90                  95
Ile Pro Phe Val Glu Thr Lys Glu Glu Ala Glu Leu Ala Val Ala Ser
            100                 105                 110
Thr Arg Tyr Pro Pro Glu Gly Ile Arg Gly Val Ser Val Ser His Arg
        115                 120                 125
Ala Asn Met Phe Gly Thr Val Ala Asp Tyr Phe Ala Gln Ser Asn Lys
    130                 135                 140
Asn Ile Thr Ile Leu Val Gln Ile Glu Ser Gln Gln Gly Val Asp Asn
145                 150                 155                 160
Val Asp Ala Ile Ala Ala Thr Glu Gly Val Asp Gly Ile Phe Val Gly
                165                 170                 175
Pro Ser Asp Leu Ala Ala Ala Leu Gly His Leu Gly Asn Ala Ser His
            180                 185                 190
Pro Asp Val Gln Lys Ala Ile Gln His Ile Phe Asn Arg Ala Ser Ala
        195                 200                 205
His Gly Lys Pro Ser Gly Ile Leu Ala Pro Val Glu Ala Asp Ala Arg
    210                 215                 220
Arg Tyr Leu Glu Trp Gly Ala Thr Phe Val Ala Val Gly Ser Asp Leu
225                 230                 235                 240
Gly Val Phe Arg Ser Ala Thr Gln Lys Leu Ala Asp Thr Phe Lys Lys
```

<210> 258
<211> 444
<212> PRT
<213> E. Coli

<400> 258

Met Ile Leu Asp Thr Val Asp Glu Lys Lys Lys Gly Val His Thr Arg
1 5 10 15
Tyr Leu Ile Leu Leu Ile Ile Phe Ile Val Thr Ala Val Asn Tyr Ala
20 25 30
Asp Arg Ala Thr Leu Ser Ile Ala Gly Thr Glu Val Ala Lys Glu Leu
35 40 45
Gln Leu Ser Ala Val Ser Met Gly Tyr Ile Phe Ser Ala Phe Gly Trp
50 55 60
Ala Tyr Leu Leu Met Gln Ile Pro Gly Gly Trp Leu Leu Asp Lys Phe
65 70 75 80
Gly Ser Lys Lys Val Tyr Thr Tyr Ser Leu Phe Phe Trp Ser Leu Pro
85 90 95
Thr Phe Leu Gln Gly Phe Val Asp Met Phe Pro Leu Ala Trp Ala Gly
100 105 110
Ile Ser Met Phe Phe Met Arg Phe Met Leu Gly Phe Ser Glu Ala Pro
115 120 125
Ser Phe Pro Ala Asn Ala Arg Ile Val Ala Ala Trp Phe Pro Thr Lys
130 135 140
Glu Arg Gly Thr Ala Ser Ala Ile Phe Asn Ser Ala Gln Tyr Phe Ser
145 150 155 160
Leu Ala Leu Phe Ser Pro Leu Leu Gly Trp Leu Thr Phe Ala Trp Gly
165 170 175
Trp Gln His Val Phe Thr Val Met Gly Val Ile Gly Phe Val Leu Thr
180 185 190
Ala Leu Trp Ile Lys Leu Ile His Asn Pro Thr Asp His Pro Arg Met
195 200 205
Ser Ala Glu Glu Leu Lys Phe Ile Ser Glu Asn Gly Ala Val Val Asp
210 215 220
Met Asp His Lys Lys Pro Gly Ser Ala Ala Ala Ser Gly Pro Lys Leu
225 230 235 240
His Tyr Ile Lys Gln Leu Leu Ser Asn Arg Met Met Leu Gly Val Pro
245 250 255
Phe Gly Gln Tyr Phe Ile Asn Thr Ile Thr Trp Phe Phe Leu Thr Trp
260 265 270
Phe Pro Ile Tyr Leu Val Gln Glu Lys Gly Met Ser Ile Leu Lys Val
275 280 285
Gly Leu Val Ala Ser Ile Pro Ala Leu Cys Gly Phe Ala Gly Gly Val
290 295 300
Leu Gly Gly Val Phe Ser Asp Tyr Leu Ile Lys Arg Gly Leu Ser Leu
305 310 315 320
Thr Leu Ala Arg Lys Leu Pro Ile Val Leu Gly Met Leu Leu Ala Ser
325 330 335
Thr Ile Ile Leu Cys Asn Tyr Thr Asn Asn Thr Thr Leu Val Val Met
340 345 350
Leu Met Ala Leu Ala Phe Phe Gly Lys Gly Phe Gly Ala Leu Gly Trp
355 360 365
Pro Val Ile Ser Asp Thr Ala Pro Lys Glu Ile Val Gly Leu Cys Gly
370 375 380

Gly Val Phe Asn Val Phe Gly Asn Val Ala Ser Ile Val Thr Pro Leu
385 390 395 400
Val Ile Gly Tyr Leu Val Ser Glu Leu His Ser Phe Asn Ala Ala Leu
405 410 415
Val Phe Val Gly Cys Ser Ala Leu Met Ala Met Val Cys Tyr Leu Phe
420 425 430
Val Val Gly Asp Ile Lys Arg Met Glu Leu Gln Lys
435 440

<210> 254
<211> 511
<212> PRT
<213> E. Coli

<400> 254
Met Gln Thr Ser Asp Thr Arg Ala Leu Pro Leu Leu Cys Ala Arg Ser
1 5 10 15
Val Tyr Lys Gln Tyr Ser Gly Val Asn Val Leu Lys Gly Ile Asp Phe
20 25 30
Thr Leu His Gln Gly Glu Val His Ala Leu Leu Gly Gly Asn Gly Ala
35 40 45
Gly Lys Ser Thr Leu Met Lys Ile Ile Ala Gly Ile Thr Pro Ala Asp
50 55 60
Ser Gly Thr Leu Glu Ile Glu Gly Asn Asn Tyr Val Arg Leu Thr Pro
65 70 75 80
Val His Ala His Gln Leu Gly Ile Tyr Leu Val Pro Gln Glu Pro Leu
85 90 95
Leu Phe Pro Asn Leu Ser Ile Lys Glu Asn Ile Leu Phe Gly Leu Ala
100 105 110
Lys Lys Gln Leu Ser Met Gln Lys Met Lys Asn Leu Leu Ala Ala Leu
115 120 125
Gly Cys Gln Phe Asp Leu His Ser Leu Ala Gly Ser Leu Asp Val Ala
130 135 140
Asp Arg Gln Met Val Glu Ile Leu Arg Gly Leu Met Arg Asp Ser Arg
145 150 155 160
Ile Leu Ile Leu Asp Glu Pro Thr Ala Ser Leu Thr Pro Ala Glu Thr
165 170 175
Gln Arg Leu Phe Ser Arg Leu Gln Glu Leu Leu Ala Thr Gly Val Gly
180 185 190
Ile Val Phe Ile Ser His Lys Leu Pro Glu Ile Arg Gln Ile Ala Asp
195 200 205
Arg Ile Ser Val Met Arg Asp Gly Thr Ile Ala Leu Ser Gly Lys Thr
210 215 220
Ser Glu Leu Ser Thr Asp Asp Ile Ile Gln Ala Ile Thr Pro Ala Val
225 230 235 240
Arg Glu Lys Ser Leu Ser Ala Ser Gln Lys Leu Trp Leu Gln Leu Pro
245 250 255
Gly Asn Arg Pro Gln His Ala Ala Gly Thr Pro Val Leu Thr Leu Glu
260 265 270
Asn Leu Thr Gly Glu Gly Phe Arg Asn Val Ser Leu Thr Leu Asn Ala
275 280 285
Gly Glu Ile Leu Gly Leu Ala Gly Leu Val Gly Ala Gly Arg Thr Glu
290 295 300
Leu Ala Glu Thr Leu Tyr Gly Leu Arg Thr Leu Arg Gly Gly Arg Ile
305 310 315 320
Met Leu Asn Gly Lys Glu Ile Asn Lys Leu Ser Thr Gly Glu Arg Leu

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                        325                                330                                335
Leu Arg Gly Leu Val Tyr Leu Pro Glu Asp Arg Gln Ser Ser Gly Leu
                    340                                345                                350
Asn Leu Asp Ala Ser Leu Ala Trp Asn Val Cys Ala Leu Thr His Asn
            355                                360                                365
Leu Arg Gly Phe Trp Ala Lys Thr Ala Lys Asp Asn Ala Thr Leu Glu
    370                                375                                380
Arg Tyr Arg Arg Ala Leu Asn Ile Lys Phe Asn Gln Pro Glu Gln Ala
385                                390                                395                                400
Ala Arg Thr Leu Ser Gly Gly Asn Gln Gln Lys Ile Leu Ile Ala Lys
                        405                                410                                415
Cys Leu Glu Ala Ser Pro Gln Val Leu Ile Val Asp Glu Pro Thr Arg
                    420                                425                                430
Gly Val Asp Val Ser Ala Arg Asn Asp Ile Tyr Gln Leu Leu Arg Ser
            435                                440                                445
Ile Ala Ala Gln Asn Val Ala Val Leu Leu Ile Ser Ser Asp Leu Glu
    450                                455                                460
Glu Ile Glu Leu Met Ala Asp Arg Val Tyr Val Met His Gln Gly Glu
465                                470                                475                                480
Ile Thr His Ser Ala Leu Thr Glu Arg Asp Ile Asn Val Glu Thr Ile
                        485                                490                                495
Met Arg Val Ala Phe Gly Asp Ser Gln Arg Gln Glu Ala Ser Cys
                    500                                505                                510


      <210> 160
      <211> [illegible]42
      <212> PRT
      <213> E. Coli

      <400> 160
Met Leu Lys Phe Ile Gln Asn Asn Arg Glu Ile Thr Ala Leu Leu Ala
 1              5                  10                  15
Val Val Leu Leu Phe Val Leu Pro Gly Phe Leu Asp Arg Gln Tyr Leu
                    20                                25                                30
Ser Val Gln Thr Leu Thr Met Val Tyr Ser Ser Ala Gln Ile Leu Ile
            35                                40                                45
Leu Leu Ala Met Gly Ala Thr Leu Val Met Leu Thr Arg Asn Ile Asp
    50                                55                                60
Val Ser Val Gly Ser Ile Thr Gly Met Cys Ala Val Leu Leu Gly Met
65                                70                                75                                80
Leu Leu Asn Ala Gly Tyr Ser Leu Pro Val Ala Cys Val Ala Thr Leu
                        85                                90                                95
Leu Leu Gly Leu Leu Ala Gly Phe Phe Asn Gly Val Leu Val Ala Trp
                    100                                105                                110
Leu Lys Ile Pro Ala Ile Val Ala Thr Leu Gly Thr Leu Gly Leu Tyr
            115                                120                                125
Arg Gly Ile Met Leu Leu Trp Thr Gly Gly Lys Trp Ile Glu Gly Leu
    130                                135                                140
Pro Ala Glu Leu Lys Gln Leu Ser Ala Pro Leu Leu Leu Gly Val Ser
145                                150                                155                                160
Ala Ile Gly Trp Leu Thr Ile Ile Leu Val Ala Phe Met Ala Trp Leu
                        165                                170                                175
Leu Ala Lys Thr Ala Phe Gly Arg Ser Phe Tyr Ala Thr Gly Asp Asn
                    180                                185                                190
Leu Gln Gly Ala Arg Gln Leu Gly Val Arg Thr Glu Ala Ile Arg Ile
            195                                200                                205
```

Val Ala Phe Ser Leu Asn Gly Cys Met Ala Ala Leu Ala Gly Ile Val
210 215 220
Phe Ala Ser Gln Ile Gly Phe Ile Pro Asn Gln Thr Gly Thr Gly Leu
225 230 235 240
Glu Met Lys Ala Ile Ala Ala Cys Val Leu Gly Gly Ile Ser Leu Leu
245 250 255
Gly Gly Ser Gly Ala Ile Ile Gly Ala Val Leu Gly Ala Trp Phe Leu
260 265 270
Thr Gln Ile Asp Ser Val Leu Val Leu Leu Arg Ile Pro Ala Trp Trp
275 280 285
Asn Asp Phe Ile Ala Gly Leu Val Leu Leu Ala Val Leu Val Phe Asp
290 295 300
Gly Arg Leu Arg Cys Ala Leu Glu Arg Asn Leu Arg Arg Gln Lys Tyr
305 310 315 320
Ala Asn Phe Met Thr Pro Pro Pro Ser Val Lys Pro Ala Ser Ser Gly
325 330 335
Lys Lys Arg Glu Ala Ala
340

<210> 261
<211> 338
<212> PRT
<213> E. Coli

<400> 261
Met Arg Ile Arg Tyr Gly Trp Glu Leu Ala Leu Ala Ala Leu Leu Val
1 5 10 15
Ile Gln Ile Val Ala Phe Gly Ala Ile Asn Pro Arg Met Leu Asp Leu
20 25 30
Asn Met Leu Leu Phe Ser Thr Ser Asp Phe Ile Cys Ile Gly Ile Val
35 40 45
Ala Leu Pro Leu Thr Met Val Ile Val Ser Gly Gly Ile Asp Ile Ser
50 55 60
Phe Gly Ser Thr Ile Gly Leu Cys Ala Ile Ala Leu Gly Val Leu Pro
65 70 75 80
Gln Ser Gly Val Pro Met Pro Leu Ala Ile Leu Leu Thr Leu Leu Leu
85 90 95
Gly Ala Leu Cys Gly Leu Ile Asn Ala Gly Leu Ile Ile Tyr Thr Lys
100 105 110
Val Asn Pro Leu Val Ile Thr Leu Gly Thr Leu Tyr Leu Phe Ala Gly
115 120 125
Ser Ala Leu Leu Leu Ser Gly Met Ala Gly Ala Thr Gly Tyr Glu Gly
130 135 140
Ile Gly Gly Phe Pro Met Ala Phe Thr Asp Phe Ala Asn Leu Asp Val
145 150 155 160
Leu Gly Leu Pro Val Pro Leu Ile Ile Phe Leu Ile Cys Leu Leu Val
165 170 175
Phe Trp Leu Trp Leu His Lys Thr His Ala Gly Arg Asn Val Phe Leu
180 185 190
Ile Gly Gln Ser Pro Arg Val Ala Leu Tyr Ser Ala Ile Pro Val Asn
195 200 205
Arg Thr Leu Cys Ala Leu Tyr Ala Met Thr Gly Leu Ala Ser Ala Val
210 215 220
Ala Ala Val Leu Leu Val Ser Tyr Phe Gly Ser Ala Arg Ser Asp Leu
225 230 235 240
Gly Ala Ser Phe Leu Met Pro Ala Ile Thr Ala Val Val Leu Gly Gly
245 250 255

Ala Asn Ile Tyr Gly Gly Ser Gly Ser Ile Ile Gly Thr Ala Ile Ala
250 265 275
Val Leu Leu Val Gly Tyr Leu Gln Gln Gly Leu Gln Met Ala Gly Val
270 280 285
Pro Asn Gln Val Ser Ser Ala Leu Ser Gly Ala Leu Leu Ile Val Val
290 295 300
Val Val Gly Asn Ser Val Ser Leu His Arg Gln Gln Ile Lys Glu Trp
305 310 315 320
Leu Ala Arg Asn Ala Asn Asn Pro Leu Pro
325 330

<210> 361
<211> 440
<212> PRT
<213> E. Coli

<400> 361
Met Thr Leu His Arg Phe Lys Lys Ile Ala Leu Leu Ser Ala Leu Gly
1 5 10 15
Ile Ala Ala Leu Ser Met Asn Val Gln Ala Ala Glu Arg Ile Ala Phe
20 25 30
Ile Pro Lys Leu Val Gly Val Gly Phe Phe Thr Ser Gly Gly Asn Gly
35 40 45
Ala Gln Thr Ala Gly Lys Glu Leu Gly Val Asp Val Thr Pyr Asp Gly
50 55 60
Pro Thr Glu Pro Ser Val Ser Gly Gln Val Gln Leu Ile Asn Asn Phe
65 70 75 80
Val Asn Thr Gly Tyr Asn Ala Ile Ile Val Ser Ala Val Ser Pro Asp
85 90 95
Gly Leu Tyr Pro Ala Leu Lys Arg Ala Met Gln Arg Gly Val Arg Val
100 105 110
Leu Thr Trp Asp Ser Asp Thr Lys Pro Glu Cys Arg Ser Tyr Tyr Ile
115 120 125
Asn Gln Gly Thr Pro Ala Gln Leu Gly Gly Met Leu Val Asp Met Ala
130 135 140
Ala Arg Thr Val Asn Lys Asp Lys Ala Lys Val Ala Phe Phe Tyr Ser
145 150 155 160
Ser Pro Thr Val Thr Asp Gln Asn Gln Trp Val Lys Glu Ala Lys Ala
165 170 175
Lys Ile Ala Lys Glu His Pro Gly Trp Glu Ile Val Thr Thr Gln Phe
180 185 190
Gly Tyr Asn Asp Ala Thr Lys Ser Leu Gln Thr Ala Glu Gly Ile Leu
195 200 205
Lys Ala Tyr Ser Asp Leu Asp Ala Ile Ile Ala Pro Asp Ala Asn Ala
210 215 220
Leu Pro Ala Ala Ala Gln Ala Ala Glu Asn Leu Lys Asn Asp Lys Val
225 230 235 240
Ala Ile Val Gly Phe Ser Thr Pro Asn Val Met Arg Pro Tyr Val Glu
245 250 255
Arg Gly Thr Val Lys Glu Phe Gly Leu Trp Asp Val Val Gln Gln Gly
260 265 270
Lys Ile Ser Val Tyr Val Ala Asp Ala Leu Leu Lys Lys Gly Ser Met
275 280 285
Lys Thr Gly Asp Lys Leu Asp Ile Lys Gly Val Gly Gln Val Glu Val

290 295 300

Ser Pro Asn Ser Val Gln Gly Tyr Asp Tyr Glu Ala Asp Gly Asn Gly
305 310 315 320
Ile Val Leu Leu Pro Glu Arg Val Ile Phe Asn Lys Glu Asn Ile Gly
325 330 335
Lys Tyr Asp Phe
340

<210> 263
<211> 341
<212> PRT
<213> E. Coli

<400> 263
Met Ala Asp Leu Asp Asp Ile Lys Asp Gly Lys Asp Phe Arg Thr Asp
1 5 10 15
Gln Pro Gln Lys Asn Ile Pro Phe Thr Leu Lys Gly Cys Gly Ala Leu
20 25 30
Asp Trp Gly Met Gln Ser Arg Leu Ser Arg Ile Phe Asn Pro Lys Thr
35 40 45
Gly Lys Thr Val Met Leu Ala Phe Asp His Gly Tyr Phe Gln Gly Pro
50 55 60
Thr Thr Gly Leu Glu Arg Ile Asp Ile Asn Ile Ala Pro Leu Phe Glu
65 70 75 80
His Ala Asp Val Leu Met Cys Thr Arg Gly Ile Leu Arg Ser Val Val
85 90 95
Pro Pro Ala Thr Asn Arg Pro Val Val Leu Arg Ala Ser Gly Ala Asn
100 105 110
Ser Ile Leu Ala Glu Leu Ser Asn Glu Ala Val Ala Leu Ser Met Asp
115 120 125
Asp Ala Val Arg Leu Asn Ser Cys Ala Val Ala Ala Gln Val Tyr Ile
130 135 140
Gly Ser Glu Tyr Glu His Gln Ser Ile Lys Asn Ile Ile Gln Leu Val
145 150 155 160
Asp Ala Gly Met Lys Val Gly Met Pro Thr Met Ala Val Thr Gly Val
165 170 175
Gly Lys Asp Met Val Arg Asp Gln Arg Tyr Phe Ser Leu Ala Thr Arg
180 185 190
Ile Ala Ala Glu Met Gly Ala Gln Ile Ile Lys Thr Tyr Tyr Val Glu
195 200 205
Lys Gly Phe Glu Arg Ile Val Ala Gly Cys Pro Val Pro Ile Val Ile
210 215 220
Ala Gly Gly Lys Lys Leu Pro Glu Arg Glu Ala Leu Glu Met Cys Trp
225 230 235 240
Gln Ala Ile Asp Gln Gly Ala Ser Gly Val Asp Met Gly Arg Asn Ile
245 250 255
Phe Gln Ser Asp His Pro Val Ala Met Met Lys Ala Val Gln Ala Val
260 265 270
Val His His Asn Glu Thr Ala Asp Arg Ala Tyr Glu Leu Tyr Leu Ser
275 280 285
Glu Lys Gln
290

<210> 264
<211> 96

<212> PRT
<213> E. Coli

<400> 164

Met His Val Thr Leu Val Glu Ile Asn Val His Glu Asp Lys Val Asp
1 5 10 15
Glu Phe Ile Glu Val Phe Arg Gln Asn His Leu Gly Ser Val Gln Glu
20 25 30
Glu Gly Asn Leu Arg Phe Asp Val Leu Gln Asp Pro Glu Val Asn Ser
35 40 45
Arg Phe Tyr Ile Tyr Glu Ala Tyr Lys Asp Glu Asp Ala Val Ala Phe
50 55 60
His Lys Thr Thr Pro His Tyr Lys Thr Cys Val Ala Lys Leu Glu Ser
65 70 75 80
Leu Met Thr Gly Pro Arg Lys Lys Arg Leu Phe Asn Gly Leu Met Pro
85 90 95

<210> 165
<211> 393
<212> PRT
<213> E. Coli

<400> 165

Met Phe Glu Pro Met Glu Leu Thr Asn Asp Ala Val Ile Lys Val Ile
1 5 10 15
Gly Val Gly Gly Gly Gly Gly Asn Ala Val Glu His Met Val Arg Glu
20 25 30
Arg Ile Glu Gly Val Glu Phe Phe Ala Val Asn Thr Asp Ala Gln Ala
35 40 45
Leu Arg Lys Thr Ala Val Gly Gln Thr Ile Gln Ile Gly Ser Gly Ile
50 55 60
Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu Val Gly Arg Asn Ala
65 70 75 80
Ala Asp Glu Asp Arg Asp Ala Leu Arg Ala Ala Leu Glu Gly Ala Asp
85 90 95
Met Val Phe Ile Ala Ala Gly Met Gly Gly Gly Thr Gly Thr Gly Ala
100 105 110
Ala Pro Val Val Ala Glu Val Ala Lys Asp Leu Gly Ile Leu Thr Val
115 120 125
Ala Val Val Thr Lys Pro Phe Asn Phe Glu Gly Lys Lys Arg Met Ala
130 135 140
Phe Ala Glu Gln Gly Ile Thr Glu Leu Ser Lys His Val Asp Ser Leu
145 150 155 160
Ile Thr Ile Pro Asn Asp Lys Leu Leu Lys Val Leu Gly Arg Gly Ile
165 170 175
Ser Leu Leu Arg Ala Phe Gly Ala Ala Asn Asp Val Leu Lys Gly Ala
180 185 190
Val Gln Gly Ile Ala Glu Leu Ile Thr Arg Pro Gly Leu Met Asn Val
195 200 205
Asp Phe Ala Asp Val Arg Thr Val Met Ser Glu Met Gly Tyr Ala Met
210 215 220
Met Gly Ser Gly Val Ala Ser Gly Glu Asp Arg Ala Glu Glu Ala Ala
225 230 235 240
Glu Met Ala Ile Ser Ser Pro Leu Leu Glu Asp Ile Asp Leu Ser Gly
245 250 255
Ala Arg Gly Val Leu Val Asn Ile Thr Ala Gly Phe Asp Leu Arg Leu

```
            260                 265                 270
Asp Glu Phe Glu Thr Val Gly Asn Thr Ile Arg Ala Phe Ala Ser Asp
        275                 280                 285
Asn Ala Thr Val Val Ile Gly Thr Ser Leu Asp Pro Asp Met Asn Asp
    290                 295                 300
Glu Leu Arg Val Thr Val Val Ala Thr Gly Ile Gly Met Asp Lys Arg
305                 310                 315                 320
Pro Glu Ile Thr Leu Val Thr Asn Lys Gln Val Gln Gln Pro Val Met
                325                 330                 335
Asp Arg Tyr Gln Gln His Gly Met Ala Pro Leu Thr Gln Glu Gln Lys
            340                 345                 350
Pro Val Ala Lys Val Val Asn Asp Asn Ala Pro Gln Thr Ala Lys Glu
        355                 360                 365
Pro Asp Tyr Leu Asp Ile Pro Ala Phe Leu Arg Lys Gln Ala Asp
    370                 375                 380
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<210> 266
<211> 1314
<212> PRT
<213> E. Coli

<400> 266

```
Met Asp Val Ser Arg Arg Gln Phe Phe Lys Ile Cys Ala Gly Gly Met
 1               5                  10                  15
Ala Gly Thr Thr Val Ala Ala Leu Gly Phe Ala Pro Lys Gln Ala Leu
            20                  25                  30
Ala Gln Ala Arg Asn Tyr Lys Leu Leu Arg Ala Lys Glu Ile Arg Asn
        35                  40                  45
Thr Cys Thr Tyr Cys Ser Val Gly Cys Gly Leu Leu Met Tyr Ser Leu
    50                  55                  60
Gly Asp Gly Ala Lys Asn Ala Arg Glu Ala Ile Tyr His Ile Glu Gly
65                  70                  75                  80
Asp Pro Asp His Pro Val Ser Arg Gly Ala Leu Cys Pro Lys Gly Ala
                85                  90                  95
Gly Leu Leu Asp Tyr Val Asn Ser Glu Asn Arg Leu Arg Tyr Pro Glu
            100                 105                 110
Tyr Arg Ala Pro Gly Ser Asp Lys Trp Gln Arg Ile Ser Trp Glu Glu
        115                 120                 125
Ala Phe Ser Arg Ile Ala Lys Leu Met Lys Ala Asp Arg Asp Ala Asn
    130                 135                 140
Phe Ile Glu Lys Asn Glu Gln Gly Val Thr Val Asn Arg Trp Leu Ser
145                 150                 155                 160
Thr Gly Met Leu Cys Ala Ser Gly Ala Ser Asn Glu Thr Gly Met Leu
                165                 170                 175
Thr Gln Lys Phe Ala Arg Ser Leu Gly Met Leu Ala Val Asp Asn Gln
            180                 185                 190
Ala Arg Val His Gly Pro Thr Val Ala Ser Leu Ala Pro Thr Phe Gly
        195                 200                 205
Arg Gly Ala Met Thr Asn His Trp Val Asp Ile Lys Asn Ala Asn Val
    210                 215                 220
Val Met Val Met Gly Gly Asn Ala Ala Glu Ala His Pro Val Gly Phe
225                 230                 235                 240
Arg Trp Ala Met Glu Ala Lys Asn Asn Asn Asp Ala Thr Leu Ile Val
                245                 250                 255
Val Asp Pro Arg Phe Thr Arg Thr Ala Ser Val Ala Asp Ile Tyr Ala
            260                 265                 270
```

Pro Ile Arg Ser Gly Thr Asp Ile Thr Phe Leu Ser Gly Val Leu Arg
275 280 285
Tyr Leu Ile Glu Asn Asn Lys Ile Asn Ala Glu Tyr Val Lys His Tyr
290 295 300
Thr Asn Ala Ser Leu Leu Val Arg Asp Asp Phe Ala Phe Glu Asp Gly
305 310 315 320
Leu Phe Ser Gly Tyr Asp Ala Glu Lys Arg Gln Tyr Asp Lys Ser Ser
325 330 335
Trp Asn Tyr Gln Leu Asp Glu Asn Gly Tyr Ala Lys Arg Asp Glu Thr
340 345 350
Leu Thr His Pro Arg Cys Val Trp Asn Leu Leu Lys Glu His Val Ser
355 360 365
Arg Tyr Thr Pro Asp Val Val Glu Asn Ile Cys Gly Thr Pro Lys Ala
370 375 380
Asp Phe Leu Lys Val Cys Glu Val Leu Ala Ser Thr Ser Ala Pro Asp
385 390 395 400
Arg Thr Thr Thr Phe Leu Tyr Ala Leu Gly Trp Thr Gln His Thr Val
405 410 415
Gly Ala Gln Asn Ile Arg Thr Met Ala Met Ile Gln Leu Leu Leu Gly
420 425 430
Asn Met Gly Met Ala Gly Gly Gly Val Asn Ala Leu Arg Gly His Ser
435 440 445
Asn Ile Gln Gly Leu Thr Asp Leu Gly Leu Leu Ser Thr Ser Leu Pro
450 455 460
Gly Tyr Leu Thr Leu Pro Ser Glu Lys Gln Val Asp Leu Gln Ser Tyr
465 470 475 480
Leu Glu Ala Asn Thr Pro Lys Ala Thr Leu Ala Asp Gln Val Asn Tyr
485 490 495
Trp Ser Asn Tyr Pro Lys Phe Phe Val Ser Leu Met Lys Ser Phe Tyr
500 505 510
Gly Asp Ala Ala Gln Lys Glu Asn Asn Trp Gly Tyr Asp Trp Leu Pro
515 520 525
Lys Trp Asp Gln Thr Tyr Asp Val Ile Lys Tyr Phe Asn Met Met Asp
530 535 540
Gln Gly Lys Val Thr Gly Tyr Phe Cys Gln Gly Phe Asn Pro Val Ala
545 550 555 560
Ser Phe Pro Asp Lys Asn Lys Val Val Ser Cys Leu Ser Lys Leu Lys
565 570 575
Tyr Met Val Val Ile Asp Pro Leu Val Thr Glu Thr Ser Thr Phe Trp
580 585 590
Gln Asn His Gly Glu Ser Asn Asp Val Asp Pro Ala Ser Ile Gln Thr
595 600 605
Glu Val Phe Arg Leu Pro Ser Thr Cys Phe Ala Glu Glu Asp Gly Ser
610 615 620
Ile Ala Asn Ser Gly Arg Trp Leu Gln Trp His Trp Lys Gly Gln Asp
625 630 635 640
Ala Pro Gly Glu Ala Arg Asn Asp Gly Glu Ile Leu Ala Gly Ile Tyr
645 650 655
His His Leu Arg Glu Leu Tyr Gln Ser Glu Gly Gly Lys Gly Val Glu
660 665 670
Pro Leu Met Lys Met Ser Trp Asn Tyr Lys Gln Pro His Glu Pro Gln
675 680 685
Ser Asp Glu Val Ala Lys Glu Asn Asn Gly Tyr Ala Leu Glu Asp Leu
690 695 700
Tyr Asp Ala Asn Gly Val Leu Ile Ala Lys Lys Gly Gln Leu Leu Ser
705 710 715 720
Ser Phe Ala His Leu Arg Asp Asp Gly Thr Thr Ala Ser Ser Cys Trp
725 730 735

```
                                725                 730                 735
Ile Tyr Thr Gly Ser Trp Thr Glu Gln Gly Asn Gln Met Ala Asn Arg
            740                 745                 750
Asp Asn Ser Asp Pro Ser Gly Leu Gly Asn Thr Leu Gly Trp Ala Trp
        755                 760                 765
Ala Trp Pro Leu Asn Arg Arg Val Leu Tyr Asn Arg Ala Ser Ala Asp
    770                 775                 780
Ile Asn Gly Lys Pro Trp Asp Pro Lys Arg Met Leu Ile Gln Trp Asn
785                 790                 795                 800
Gly Ser Lys Trp Thr Gly Asn Asp Ile Pro Asp Phe Gly Asn Ala Ala
                805                 810                 815
Pro Gly Thr Pro Thr Gly Pro Phe Ile Met Gln Pro Glu Gly Met Gly
            820                 825                 830
Arg Leu Phe Ala Ile Asn Lys Met Ala Glu Gly Pro Phe Pro Glu His
        835                 840                 845
Tyr Glu Pro Ile Glu Thr Pro Leu Gly Thr Asn Pro Leu His Pro Asn
    850                 855                 860
Val Val Ser Asn Pro Val Val Arg Leu Tyr Glu Gln Asp Ala Leu Arg
865                 870                 875                 880
Met Gly Lys Lys Glu Gln Phe Pro Tyr Val Gly Thr Thr Tyr Arg Leu
                885                 890                 895
Thr Glu His Phe His Thr Trp Thr Lys His Ala Leu Leu Asn Ala Ile
            900                 905                 910
Ala Gln Pro Glu Gln Phe Val Glu Ile Ser Glu Thr Leu Ala Ala Ala
        915                 920                 925
Lys Gly Ile Asn Asn Gly Asp Arg Val Thr Val Ser Ser Lys Arg Gly
    930                 935                 940
Ile Arg Ala Val Ala Val Val Thr Arg Arg Leu Lys Pro Leu Asn
945                 950                 955                 960
Val Asn Gly Gln Gln Val Glu Thr Val Gly Ile Pro Ile His Trp Gly
                965                 970                 975
Phe Glu Gly Val Ala Arg Lys Gly Tyr Ile Ala Asn Thr Leu Thr Pro
            980                 985                 990
Asn Val Gly Asp Ala Asn Ser Gln Thr Pro Glu Tyr Lys Ala Phe Leu
        995                 1000                1005
Val Asn Ile Glu Lys Ala
    1010
```

<213> 267
<211> 344
<212> PRT
<213> E. Coli

<400> 267

```
Met Ala Met Glu Thr Gln Asp Ile Ile Lys Arg Ser Ala Thr Asn Ser
 1               5                  10                  15
Ile Thr Pro Pro Ser Gln Val Arg Asp Tyr Lys Ala Glu Val Ala Lys
            20                  25                  30
Leu Ile Asp Val Ser Thr Cys Ile Gly Cys Lys Ala Cys Glu Val Ala
        35                  40                  45
Cys Ser Glu Trp Asn Asp Ile Arg Asp Glu Val Gly His Cys Val Gly
    50                  55                  60
Val Tyr Asp Asn Pro Ala Asp Leu Ser Ala Lys Ser Trp Thr Val Met
65                  70                  75                  80
Arg Phe Ser Glu Thr Glu Gln Asn Gly Lys Leu Glu Trp Leu Ile Arg
                85                  90                  95
Lys Asp Gly Cys Met His Cys Glu Asp Pro Gly Cys Leu Lys Ala Cys
            100                 105                 110
```

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                    100                 105                 110
Pro Ser Ala Gly Ala Ile Ile Gln Tyr Ala Asn Gly Ile Val Asp Phe
            115                 120                 125
Gln Ser Glu Asn Cys Ile Gly Cys Gly Tyr Cys Ile Ala Gly Cys Pro
        130                 135                 140
Phe Asn Ile Pro Arg Leu Asn Lys Glu Asp Asn Arg Val Tyr Lys Cys
145                 150                 155                 160
Thr Leu Cys Val Asp Arg Val Ser Val Gly Gln Glu Pro Ala Cys Val
                165                 170                 175
Lys Thr Cys Pro Thr Gly Ala Ile His Phe Gly Thr Lys Lys Glu Met
            180                 185                 190
Leu Glu Leu Ala Glu Gln Arg Val Ala Lys Leu Lys Ala Arg Gly Tyr
        195                 200                 205
Glu His Ala Gly Val Tyr Asn Pro Glu Gly Val Gly Gly Thr His Val
    210                 215                 220
Met Tyr Val Leu His His Ala Asp Gln Pro Glu Leu Tyr His Gly Leu
225                 230                 235                 240
Pro Lys Asp Pro Lys Ile Asp Thr Ser Val Ser Leu Trp Lys Gly Ala
                245                 250                 255
Leu Lys Pro Leu Ala Ala Ala Gly Phe Ile Ala Thr Phe Ala Gly Leu
            260                 265                 270
Ile Phe His Tyr Ile Gly Ile Gly Pro Asn Lys Glu Val Asp Asp Asp
        275                 280                 285
Ala Glu Asp His His Glu
    290
```



```
Met Ser Lys Ser Lys Met Ile Val Arg Thr Lys Phe Ile Asp Arg Ala
 1               5                  10                  15
Cys His Trp Thr Val Val Ile Cys Phe Phe Leu Val Ala Leu Ser Gly
            20                  25                  30
Ile Ser Phe Phe Phe Pro Thr Leu Gln Trp Leu Thr Gln Thr Phe Gly
        35                  40                  45
Thr Pro Gln Met Gly Arg Ile Leu His Pro Phe Phe Gly Ile Ala Ile
    50                  55                  60
Phe Val Ala Leu Met Phe Met Phe Val Arg Phe Val His His Asn Ile
65                  70                  75                  80
Pro Asp Lys Lys Asp Ile Pro Trp Leu Leu Asn Ile Val Glu Val Leu
                85                  90                  95
Lys Gly Asn Glu His Lys Val Ala Asp Val Gly Lys Tyr Asn Ala Gly
            100                 105                 110
Gln Lys Met Met Phe Trp Ser Ile Met Ser Met Ile Phe Val Leu Leu
        115                 120                 125
Val Thr Gly Val Ile Ile Trp Arg Pro Tyr Phe Ala Gln Tyr Phe Pro
    130                 135                 140
Met Gln Val Val Arg Tyr Ser Leu Leu Ile His Ala Ala Ala Gly Ile
145                 150                 155                 160
Ile Leu Ile His Ala Ile Leu Ile His Met Tyr Met Ala Phe Trp Val
                165                 170                 175
Lys Gly Ser Ile Lys Gly Met Ile Glu Gly Lys Val Ser Arg Arg Trp
            180                 185                 190
```

Ala Lys Lys His His Pro Arg Trp Tyr Arg Glu Ile Glu Lys Ala Glu
195 200 205
Ala Lys Lys Glu Ser Glu Glu Gly Ile
210 215

<210> 269
<211> 86
<212> PRT
<213> E. Coli

<400> 269
Met Ala Leu Leu Ile Thr Lys Lys Cys Ile Asn Cys Asp Met Cys Glu
1 5 10 15
Pro Glu Cys Pro Asn Glu Ala Ile Ser Met Gly Asp His Ile Tyr Glu
20 25 30
Ile Asn Ser Asp Lys Cys Thr Glu Cys Val Gly His Tyr Glu Thr Pro
35 40 45
Thr Cys Gln Lys Val Cys Pro Ile Pro Asn Thr Ile Val Lys Asp Pro
50 55 60
Ala His Val Glu Thr Glu Glu Gln Leu Trp Asp Lys Phe Val Leu Met
65 70 75 80
His His Ala Asp Lys Ile
85

<210> 270
<211> 403
<212> PRT
<213> E. Coli

<400> 270
Met Gln Ser Val Asp Val Ala Ile Val Gly Gly Gly Met Val Gly Leu
1 5 10 15
Ala Val Ala Cys Gly Leu Gln Gly Ser Gly Leu Arg Val Ala Val Leu
20 25 30
Glu Gln Arg Val Gln Glu Pro Leu Ala Ala Asn Ala Pro Pro Gln Leu
35 40 45
Arg Val Ser Ala Ile Asn Ala Ala Ser Glu Lys Leu Leu Thr Arg Leu
50 55 60
Gly Val Trp Gln Asp Ile Leu Ser Arg Arg Ala Ser Cys Tyr His Gly
65 70 75 80
Met Gln Val Trp Asp Lys Asp Ser Phe Gly His Ile Ser Phe Asp Asp
85 90 95
Gln Ser Met Gly Tyr Ser His Leu Gly His Ile Val Glu Asn Ser Val
100 105 110
Ile His Tyr Ala Leu Trp Asn Lys Ala His Gln Ser Ser Asp Ile Thr
115 120 125
Leu Leu Ala Pro Ala Glu Leu Gln Gln Val Ala Trp Gly Glu Asn Glu
130 135 140
Thr Phe Leu Thr Leu Lys Asp Gly Ser Met Leu Thr Ala Arg Leu Val
145 150 155 160
Ile Gly Ala Asp Gly Ala Asn Ser Trp Leu Arg Asn Lys Ala Asp Ile
165 170 175
Pro Leu Thr Phe Trp Asp Tyr Gln His His Ala Leu Val Ala Thr Ile
180 185 190
Arg Thr Glu Glu Pro His Asp Ala Val Ala Arg Gln Val Phe His Gly

```
          195                 200                 205
Glu Gly Ile Leu Ala Phe Leu Pro Leu Ser Asp Pro His Leu Cys Ser
    210                 215                 220
Ile Val Trp Ser Leu Ser Pro Glu Glu Ala Gln Arg Met Gln Gln Ala
225                 230                 235                 240
Ser Glu Asp Glu Phe Asn Arg Ala Leu Asn Ile Ala Phe Asp Asn Arg
                245                 250                 255
Leu Gly Leu Cys Lys Val Glu Ser Ala Arg Gln Val Phe Pro Leu Thr
            260                 265                 270
Gly Arg Tyr Ala Arg Gln Phe Ala Ser His Arg Leu Ala Leu Val Gly
        275                 280                 285
Asp Ala Ala His Thr Ile His Pro Leu Ala Gly Gln Gly Val Asn Leu
    290                 295                 300
Gly Phe Met Asp Ala Ala Glu Leu Ile Ala Glu Leu Lys Arg Leu His
305                 310                 315                 320
Arg Gln Gly Lys Asp Ile Gly Gln Tyr Ile Tyr Leu Arg Arg Tyr Glu
                325                 330                 335
Arg Ser Arg Lys His Ser Ala Ala Leu Met Leu Ala Gly Met Gln Gly
            340                 345                 350
Phe Arg Asp Leu Phe Ser Gly Thr Asn Pro Ala Lys Lys Leu Leu Arg
        355                 360                 365
Asp Ile Gly Leu Lys Leu Ala Asp Thr Leu Pro Gly Val Lys Pro Gln
    370                 375                 380
Leu Ile Arg Gln Ala Met Gly Leu Asn Asp Leu Pro Glu Trp Leu Arg
385                 390                 395                 400
```

<211> 171
<211> aa
<212> PRT
<213> E. Coli

<400> 271

```
Met Ser Val Ile Ile Val Gly Gly Gly Met Ala Gly Ala Thr Leu Ala
 1               5                  10                  15
Leu Ala Ile Ser Arg Leu Ser His Gly Ala Leu Pro Val His Leu Ile
            20                  25                  30
Glu Ala Thr Ala Pro Glu Ser His Ala His Pro Gly Phe Asp Gly Arg
        35                  40                  45
Ala Ile Ala Leu Ala Ala Gly Thr Cys Gln Gln Leu Ala Arg Ile Gly
    50                  55                  60
Val Trp Gln Ser Leu Ala Asp Cys Ala Thr Ala Ile Thr Thr Val His
65                  70                  75                  80
Val Ser Asp Arg Gly His Ala Gly Phe Val Thr Leu Ala Ala Glu Asp
                85                  90                  95
Tyr Gln Leu Ala Ala Leu Gly Gln Val Val Glu Leu His Asn Val Gly
            100                 105                 110
Gln Arg Leu Phe Ala Leu Leu Arg Lys Ala Pro Gly Val Thr Leu His
        115                 120                 125
Cys Pro Asp Arg Val Ala Asn Val Ala Arg Thr Gln Ser His Val Glu
    130                 135                 140
Val Thr Leu Glu Ser Gly Glu Thr Leu Thr Gly Arg Val Leu Val Ala
145                 150                 155                 160
Ala Asp Gly Thr His Ser Ala Leu Ala Thr Ala Cys Gly Val Asp Trp
                165                 170                 175
Gln Gln Glu Pro Tyr Glu Gln Leu Ala Val Ile Ala Asn Val Ala Thr
            180                 185                 190
```

Ser Val Ala His Glu Gly Arg Ala Phe Glu Arg Phe Thr Gln His Gly
145 200 205
Pro Leu Ala Met Leu Pro Met Ser Asp Gly Arg Cys Ser Leu Val Trp
210 215 220
Cys His Pro Leu Glu Arg Arg Glu Glu Val Leu Ser Trp Ser Asp Glu
225 230 235 240
Lys Phe Cys Arg Glu Leu Gln Ser Ala Phe Gly Trp Arg Leu Gly Lys
245 250 255
Ile Thr His Ala Gly Lys Arg Ser Ala Tyr Pro Leu Ala Leu Thr His
260 265 270
Ala Ala Arg Ser Ile Thr His Arg Thr Val Leu Val Gly Asn Ala Ala
275 280 285
Gln Thr Leu His Pro Ile Ala Gly Gln Gly Phe Asn Leu Gly Met Arg
290 295 300
Asp Val Met Ser Leu Ala Glu Thr Leu Thr Gln Ala Gln Glu Arg Gly
305 310 315 320
Glu Asp Met Gly Asp Tyr Gly Val Leu Cys Arg Tyr Gln Gln Arg Arg
325 330 335
Gln Ser Asp Arg Glu Ala Thr Ile Gly Val Thr Asp Ser Leu Val His
340 345 350
Leu Phe Ala Asn Arg Trp Ala Pro Leu Val Val Gly Arg Asn Ile Gly
355 360 365
Leu Met Thr Met Glu Leu Phe Thr Pro Ala Arg Asp Val Leu Ala Gln
370 375 380
Arg Thr Leu Gly Trp Val Ala Arg
385 390

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids

(B) TYPE: PRT

(C) STRANDEDNESS: E. Coli

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Glu Ile Ser Arg Thr Gly Phe Gln Arg Arg Arg Gln Ala Leu
1 5 10 15
Val Glu Gln Met Gln Pro Gly Ser Ala Ala Leu Ile Phe Ala Ala Pro
20 25 30
Glu Val Thr Arg Ser Ala Asp Ser Glu Tyr Pro Tyr Arg Gln Asn Ser
35 40 45
Asp Phe Trp Tyr Phe Thr Gly Phe Asn Glu Pro Glu Ala Val Leu Val
50 55 60
Leu Ile Lys Ser Asp Asp Thr His Asn His Ser Val Leu Phe Asn Arg
65 70 75 80
Val Arg Asp Leu Thr Ala Glu Ile Trp Phe Gly Arg Arg Leu Gly Gln
85 90 95
Asp Ala Ala Pro Glu Lys Leu Gly Val Asp Arg Ala Leu Ala Phe Ser
100 105 110
Glu Ile Asn Gln Gln Leu Tyr Gln Leu Leu Asn Gly Leu Asp Val Val
115 120 125
Tyr His Ala Gln Gly Glu Tyr Ala Tyr Ala Asp Val Ile Val Asn Ser
130 135 140
Ala Leu Glu Lys Leu Arg Lys Gly Ser Arg Gln Leu Thr Ala Pro
145 150 155 160
Ala Thr Met Ile Asp Trp Arg Pro Val Val His Glu Met Arg Leu Phe
165 170 175
Lys Ser Pro Glu Glu Ile Ala Val Leu Arg Arg Ala Gly Glu Ile Thr

```
                180                 185                 190
Ala Met Ala His Thr Arg Ala Met Glu Lys Cys Arg Pro Gly Met Phe
        195                 200                 205
Glu Tyr His Leu Glu Gly Glu Ile His His Glu Phe Asn Arg His Gly
    210                 215                 220
Ala Arg Tyr Pro Ser Tyr Asn Thr Ile Val Gly Ser Gly Glu Asn Gly
225                 230                 235                 240
Cys Ile Leu His Tyr Thr Glu Asn Glu Cys Glu Met Arg Asp Gly Asp
                245                 250                 255
Leu Val Leu Ile Asp Ala Gly Cys Glu Tyr Lys Gly Tyr Ala Gly Asp
            260                 265                 270
Ile Thr Arg Thr Phe Pro Val Asn Gly Lys Phe Thr Gln Ala Gln Arg
        275                 280                 285
Glu Ile Tyr Asp Ile Val Leu Glu Ser Leu Glu Thr Ser Leu Arg Leu
    290                 295                 300
Tyr Asn Pro Gly Thr Ser Ile Leu Glu Val Thr Gly Glu Val Val Arg
305                 310                 315                 320
Ile Met Val Ser Gly Leu Val Lys Leu Gly Ile Leu Lys Gly Asp Val
                325                 330                 335
Asp Glu Leu Ile Ala Gln Asn Ala His Arg Pro Phe Phe Met His Gly
            340                 345                 350
Leu Ser His Trp Leu Gly Leu Asp Val His Asp Val Gly Val Tyr Gly
        355                 360                 365
Gln Asp Arg Ser Arg Ile Leu Glu Pro Gly Met Val Leu Thr Val Glu
    370                 375                 380
Pro Gly Leu Tyr Ile Ala Pro Asp Ala Glu Val Pro Glu Gln Tyr Arg
385                 390                 395                 400
Gly Ile Gly Ile Arg Ile Glu Asp Asp Ile Val Ile Thr Glu Thr Gly
                405                 410                 415
Asn Glu Asn Leu Thr Ala Ser Val Val Lys Lys Pro Glu Glu Ile Glu
            420                 425                 430
Ala Leu Met Val Ala Ala Arg Lys Gln
        435                 440
```


<210> 273
<211> 194
<212> PRT
<213> E. Coli

<400> 273

```
Met Leu Met Ser Ile Gln Asn His Met Pro Gly Tyr Asn Glu Met Asn
 1               5                  10                  15
Gln Tyr Leu Asn Gln Gln Gly Thr Gly Leu Thr Pro Ala Glu Met His
            20                  25                  30
Gly Leu Ile Ser Gly Met Ile Cys Gly Gly Asn Asp Asp Ser Ser Trp
        35                  40                  45
Leu Pro Leu Leu His Asp Leu Thr Asn Glu Gly Met Ala Phe Gly His
    50                  55                  60
Glu Leu Ala Gln Ala Leu Arg Lys Met His Ser Ala Thr Ser Asp Ala
65                  70                  75                  80
Leu Gln Asp Asp Gly Phe Leu Phe Gln Leu Tyr Leu Pro Asp Gly Asp
                85                  90                  95
Asp Val Ser Val Phe Asp Arg Ala Asp Ala Leu Ala Gly Trp Val Asn
            100                 105                 110
His Phe Leu Leu Gly Leu Gly Val Thr Gln Pro Lys Leu Asp Lys Val
        115                 120                 125
```

Thr Gly Glu Thr Gly Glu Ala Ile Asp Asp Leu Arg Asn Ile Ala Gln
130 135 140
Leu Gly Tyr Asp Glu Asp Glu Asp Gln Glu Glu Leu Glu Met Ser Leu
145 150 155 160
Glu Glu Ile Ile Glu Tyr Val Arg Val Ala Ala Leu Leu Cys His Asp
165 170 175
Thr Phe Thr His Pro Gln Pro Thr Ala Pro Glu Val Gln Lys Pro Thr
180 185 190
Leu His

<210> 174
<211> 129
<212> PRT
<213> E. Coli

<400> 174
Met Leu Lys Leu Phe Ala Lys Tyr Thr Ser Ile Gly Val Leu Asn Thr
1 5 10 15
Leu Ile His Trp Val Val Phe Gly Val Cys Ile Tyr Val Ala His Thr
20 25 30
Asn Gln Ala Leu Ala Asn Phe Ala Gly Phe Val Val Ala Val Ser Phe
35 40 45
Ser Phe Phe Ala Asn Ala Lys Phe Thr Phe Lys Ala Ser Thr Thr Thr
50 55 60
Met Arg Tyr Met Leu Tyr Val Gly Phe Met Gly Thr Leu Ser Ala Thr
65 70 75 80
Val Gly Trp Ala Ala Asp Arg Cys Ala Leu Pro Pro Met Ile Thr Leu
85 90 95
Val Thr Phe Ser Ala Ile Ser Leu Val Cys Gly Phe Val Tyr Ser Lys
100 105 110
Phe Ile Val Phe Arg Asp Ala Lys
115 120

<210> 175
<211> 136
<212> PRT
<213> E. Coli

<400> 175
Met Lys Ile Ser Leu Val Val Pro Val Phe Asn Glu Glu Glu Ala Ile
1 5 10 15
Pro Ile Phe Tyr Lys Thr Val Arg Glu Phe Glu Glu Leu Lys Ser Tyr
20 25 30
Glu Val Glu Ile Val Phe Ile Asn Asp Gly Ser Lys Asp Ala Thr Glu
35 40 45
Ser Ile Ile Asn Ala Leu Ala Val Ser Asp Pro Leu Val Val Pro Leu
50 55 60
Ser Phe Thr Arg Asn Phe Gly Lys Glu Pro Ala Leu Phe Ala Gly Leu
65 70 75 80
Asp His Ala Thr Gly Asp Ala Ile Ile Pro Ile Asp Val Asp Leu Gln
85 90 95
Asp Pro Ile Glu Val Ile Pro His Leu Ile Glu Lys Trp Gln Ala Gly
100 105 110
Ala Asp Met Val Leu Ala Lys Arg Ser Asp Arg Ser Thr Asp Gly Arg
115 120 125

Leu Lys Arg Lys Thr Ala Glu Trp Phe Tyr Lys Leu His Asn Lys Ile
130 135 140

Ser Asn Pro Lys Ile Glu Glu Asn Val Gly Asp Phe Arg Leu Met Ser
145 150 155 160

Arg Asp Val Val Glu Asn Ile Lys Leu Met Pro Glu Arg Asn Leu Phe
165 170 175

Met Lys Gly Ile Leu Ser Trp Val Gly Gly Lys Thr Asp Ile Val Glu
180 185 190

Tyr Val Arg Ala Glu Arg Ile Ala Gly Asp Thr Lys Phe Asn Gly Trp
195 200 205

Lys Leu Trp Asn Leu Ala Leu Glu Gly Ile Thr Ser Phe Ser Thr Phe
210 215 220

Pro Leu Arg Ile Trp Thr Tyr Ile Gly Leu Val Val Ala Ser Val Ala
225 230 235 240

Phe Ile Tyr Gly Ala Trp Met Ile Leu Asp Thr Ile Ile Phe Gly Asn
245 250 255

Ala Val Arg Gly Tyr Pro Ser Leu Leu Val Ser Ile Leu Phe Leu Gly
260 265 270

Gly Ile Gln Met Ile Gly Ile Gly Val Leu Gly Glu Tyr Ile Gly Arg
275 280 285

Thr Tyr Ile Glu Thr Lys Lys Arg Pro Lys Tyr Ile Ile Lys Arg Val
290 295 300

Lys Lys
305

<210> 276
<211> 443
<212> PRT
<213> E. Coli

<400> 276

Met Asn Lys Ala Ile Lys Val Ser Leu Tyr Ile Ser Phe Val Leu Ile
1 5 10 15

Ile Cys Ala Leu Ser Lys Asn Ile Met Met Leu Asn Thr Ser Asp Phe
20 25 30

Gly Arg Ala Ile Lys Pro Leu Ile Glu Asp Ile Pro Ala Phe Thr Tyr
35 40 45

Asp Leu Pro Leu Leu Tyr Lys Leu Lys Gly His Ile Asp Ser Ile Asp
50 55 60

Ser Tyr Glu Tyr Ile Ser Ser Tyr Ser Tyr Ile Leu Tyr Thr Tyr Val
65 70 75 80

Leu Phe Ile Ser Ile Phe Thr Glu Tyr Leu Asp Ala Arg Val Leu Ser
85 90 95

Leu Phe Leu Lys Val Ile Tyr Ile Tyr Ser Leu Tyr Ala Ile Phe Thr
100 105 110

Ser Tyr Ile Lys Thr Glu Arg Tyr Val Thr Leu Phe Thr Phe Phe Ile
115 120 125

Leu Ala Phe Leu Met Cys Ser Ser Ser Thr Leu Ser Met Phe Ala Ser
130 135 140

Phe Tyr Gln Glu Gln Ile Val Ile Ile Phe Leu Pro Phe Leu Val Tyr
145 150 155 160

Ser Leu Thr Cys Lys Asn Asn Lys Ser Met Leu Leu Leu Phe Phe Ser
165 170 175

Leu Leu Ile Ile Ser Thr Ala Lys Asn Gln Phe Ile Leu Thr Pro Leu
180 185 190

Ile Val Tyr Ser Tyr Tyr Ile Phe Phe Asp Arg His Lys Leu Ile Ile

195 200 205
Lys Ser Val Ile Cys Val Val Cys Leu Leu Ala Ser Ile Phe Ala Ile
210 215 220
Ser Tyr Ser Lys Gly Val Val Glu Leu Asn Lys Tyr His Ala Thr Tyr
225 230 235 240
Phe Gly Ser Tyr Leu Tyr Met Lys Asn Asn Gly Tyr Lys Met Pro Ser
245 250 255
Tyr Val Asp Asp Lys Cys Val Gly Leu Asp Ala Trp Gly Asn Lys Phe
260 265 270
Asp Ile Ser Phe Gly Ala Thr Pro Thr Glu Val Gly Thr Glu Cys Phe
275 280 285
Glu Ser His Lys Asp Glu Thr Phe Ser Asn Ala Leu Phe Leu Leu Val
290 295 300
Ser Lys Pro Ser Thr Ile Phe Lys Leu Pro Phe Asp Asp Gly Val Met
305 310 315 320
Ser Gln Tyr Lys Glu Asn Tyr Phe His Val Tyr Lys Lys Leu His Val
325 330 335
Ile Tyr Gly Glu Ser Asn Ile Leu Thr Thr Ile Thr Asn Ile Lys Asp
340 345 350
Asn Ile Phe Lys Asn Ile Arg Phe Ile Ser Leu Leu Leu Phe Phe Ile
355 360 365
Ala Ser Ile Phe Ile Arg Asn Asn Lys Ile Lys Ala Ser Leu Phe Val
370 375 380
Val Ser Leu Phe Gly Ile Ser Gln Phe Tyr Val Ser Phe Phe Gly Glu
385 390 395 400
Gly Tyr Arg Asp Leu Ser Lys His Leu Phe Gly Met Tyr Phe Ser Phe
405 410 415
Asp Leu Cys Leu Tyr Ile Thr Val Val Phe Leu Ile Tyr Lys Ile Ile
420 425 430
Gln Arg Asn Gln Asp Asn Ser Asp Val Lys His
435 440

<210> 177
<211> 82
<212> PRT
<213> E. Coli

<400> 177
Met Gly Ile Leu Ser Trp Ile Ile Phe Gly Leu Ile Ala Gly Ile Leu
1 5 10 15
Ala Lys Trp Ile Met Pro Gly Lys Asp Gly Gly Gly Phe Phe Met Thr
20 25 30
Ile Leu Leu Gly Ile Val Gly Ala Val Val Gly Gly Trp Ile Ser Thr
35 40 45
Leu Phe Gly Phe Gly Lys Val Asp Gly Phe Asn Phe Gly Ser Phe Val
50 55 60
Val Ala Val Ile Gly Ala Ile Val Val Leu Phe Ile Tyr Arg Lys Ile
65 70 75 80
Lys Ser

<210> 178
<211> 6[illegible]
<212> PRT

<213> E. Coli

<400> 378

Met	Gly	Lys	Ala	Thr	Tyr	Thr	Val	Thr	Val	Thr	Asn	Asn	Ser	Asn	Gly
1				5				10					15		
Val	Ser	Val	Asp	Tyr	Glu	Thr	Glu	Thr	Pro	Met	Thr	Leu	Leu	Val	Pro
			20				25					30			
Glu	Val	Ala	Ala	Glu	Val	Ile	Lys	Asp	Leu	Val	Asn	Thr	Val	Arg	Ser
		35					40					45			
Tyr	Asp	Thr	Glu	Asn	Glu	His	Asp	Val	Cys	Gly	Trp				
	50					55					60				

<210> 379
<211> 119
<212> PRT
<213> E. Coli

<400> 379

Met	Leu	Gln	Ile	Pro	Gln	Asn	Tyr	Ile	His	Thr	Arg	Ser	Thr	Pro	Phe
1				5				10					15		
Trp	Asn	Lys	Gln	Thr	Ala	Pro	Ala	Gly	Ile	Phe	Glu	Arg	His	Leu	Asp
			20				25					30			
Lys	Gly	Thr	Arg	Pro	Gly	Val	Tyr	Pro	Arg	Leu	Ser	Val	Met	His	Gly
		35					40					45			
Ala	Val	Lys	Tyr	Leu	Gly	Tyr	Ala	Asp	Glu	His	Ser	Ala	Glu	Pro	Asp
	50					55					60				
Gln	Val	Ile	Leu	Ile	Glu	Ala	Gly	Gln	Phe	Ala	Val	Phe	Pro	Pro	Glu
65					70					75					80
Lys	Trp	His	Asn	Ile	Glu	Ala	Met	Thr	Asp	Asp	Thr	Tyr	Phe	Asn	Ile
				85					90					95	
Asp	Phe	Phe	Val	Ala	Pro	Glu	Val	Leu	Met	Glu	Gly	Ala	Gln	Gln	Arg
			100					105					110		
Lys	Val	Ile	His	Asn	Gly	Lys									
		115													

<210> 380
<211> 436
<212> PRT
<213> E. Coli

<400> 380

Met	Lys	Phe	Lys	Val	Ile	Ala	Leu	Ala	Ala	Leu	Met	Gly	Ile	Ser	Gly
1				5				10					15		
Met	Ala	Ala	Gln	Ala	Asn	Glu	Leu	Pro	Asp	Gly	Pro	His	Ile	Val	Thr
			20				25					30			
Ser	Gly	Thr	Ala	Ser	Val	Asp	Ala	Val	Pro	Asp	Ile	Ala	Thr	Leu	Ala
		35					40					45			
Ile	Gln	Val	Asn	Val	Ala	Ala	Lys	Asp	Ala	Ala	Thr	Ala	Lys	Lys	Gln
	50					55					60				
Ala	Asp	Gln	Arg	Val	Ala	Gln	Tyr	Ile	Ser	Phe	Leu	Glu	Leu	Asn	Gln
65					70					75					80
Ile	Ala	Lys	Lys	Asp	Ile	Ser	Ser	Ala	Asn	Leu	Arg	Thr	Gln	Pro	Asp
				85					90					95	
Tyr	Asp	Tyr	Gln	Asp	Gly	Lys	Ser	Ile	Leu	Lys	Gly	Tyr	Arg	Ala	Val
			100					105					110		

Arg Thr Val Glu Val Thr Leu Arg Gln Leu Asp Lys Leu Asn Ser Leu
115 120 125
Leu Asp Gly Ala Leu Lys Ala Gly Leu Asn Glu Ile Arg Ser Val Ser
130 135 140
Leu Gly Val Ala Gln Pro Asp Ala Tyr Lys Asp Lys Ala Arg Lys Ala
145 150 155 160
Ala Ile Asp Asn Ala Ile His Gln Ala Gln Glu Leu Ala Asn Gly Phe
165 170 175
His Arg Lys Leu Gly Pro Val Tyr Ser Val Arg Tyr His Val Ser Asn
180 185 190
Tyr Gln Pro Ser Pro Met Val Arg Met Met Lys Ala Asp Ala Ala Pro
195 200 205
Val Ser Ala Gln Glu Thr Tyr Glu Gln Ala Ala Ile Gln Phe Asp Asp
210 215 220
Gln Val Asp Val Val Phe Gln Leu Glu Pro Val Asp Gln Gln Pro Ala
225 230 235 240
Lys Thr Pro Ala Ala Gln
245

<210> 281
<211> 464
<212> PRT
<213> E. Coli

<400> 281
Met Leu Leu Leu Asp Ala Cys Ser Gln Met Cys Pro Ser Phe Arg Arg
1 5 10 15
Phe Gln Thr Val Phe His Asn Ser Ser Ile Phe Leu Pro Tyr Trp Leu
20 25 30
Ala Thr Leu Val Ser Phe Arg Glu Thr Phe Gln Glu Glu Lys Leu Leu
35 40 45
Thr Met Lys Gly Ser Tyr Lys Ser Arg Trp Val Ile Val Ile Val Val
50 55 60
Val Ile Ala Ala Ile Ala Ala Phe Trp Phe Trp Gln Gly Arg Asn Asp
65 70 75 80
Ser Arg Ser Ala Ala Pro Gly Ala Thr Lys Gln Ala Gln Gln Ser Pro
85 90 95
Ala Gly Gly Arg Arg Gly Met Arg Ser Gly Pro Leu Ala Pro Val Gln
100 105 110
Ala Ala Thr Ala Val Glu Gln Ala Val Pro Arg Tyr Leu Thr Gly Leu
115 120 125
Gly Thr Ile Thr Ala Ala Asn Thr Val Thr Val Arg Ser Arg Val Asp
130 135 140
Gly Gln Leu Ile Ala Leu His Phe Gln Glu Gly Gln Gln Val Lys Ala
145 150 155 160
Gly Asp Leu Leu Ala Glu Ile Asp Pro Ser Gln Phe Lys Val Ala Leu
165 170 175
Ala Gln Ala Gln Gly Gln Leu Ala Lys Asp Lys Ala Thr Leu Ala Asn
180 185 190
Ala Arg Arg Asp Leu Ala Arg Tyr Gln Gln Leu Ala Lys Thr Asn Leu
195 200 205
Val Ser Arg Gln Glu Leu Asp Ala Gln Gln Ala Leu Val Ser Glu Thr
210 215 220
Glu Gly Thr Ile Lys Ala Asp Glu Ala Ser Val Ala Ser Ala Gln Leu
225 230 235 240
Gln Leu Asp Trp Ser Arg Ile Thr Ala Pro Val Asp Gly Arg Val Gly

```
                                245                 250                 255
Leu Lys Gln Val Asp Val Gly Asn Gln Ile Ser Ser Gly Asp Thr Thr
            260                 265                 270
Gly Ile Val Val Ile Thr Gln Thr His Pro Ile Asp Leu Val Phe Thr
        275                 280                 285
Leu Pro Glu Ser Asp Ile Ala Thr Val Val Gln Ala Gln Lys Ala Gly
    290                 295                 300
Lys Pro Leu Val Val Glu Ala Trp Asp Arg Thr Asn Ser Lys Lys Leu
305                 310                 315                 320
Ser Glu Gly Thr Leu Leu Ser Leu Asp Asn Gln Ile Asp Ala Thr Thr
                325                 330                 335
Gly Thr Ile Lys Val Lys Ala Arg Phe Asn Asn Gln Asp Asp Ala Leu
            340                 345                 350
Phe Pro Asn Gln Phe Val Asn Ala Arg Met Leu Val Asp Thr Glu Gln
        355                 360                 365
Asn Ala Val Val Ile Pro Thr Ala Ala Leu Gln Met Gly Asn Glu Gly
    370                 375                 380
His Phe Val Trp Val Leu Asn Ser Glu Asn Lys Val Ser Lys His Leu
385                 390                 395                 400
Val Thr Pro Gly Ile Gln Asp Ser Gln Lys Val Val Ile Arg Ala Gly
                405                 410                 415
Ile Ser Ala Gly Asp Arg Val Val Thr Asp Gly Ile Asp Arg Leu Thr
            420                 425                 430
Glu Gly Ala Lys Val Glu Val Val Glu Ala Gln Ser Ala Thr Thr Pro
        435                 440                 445
Glu Glu Lys Ala Thr Ser Arg Glu Tyr Ala Lys Lys Gly Ala Arg Ser
    450                 455                 460
```


(210) 161

(211) 1040

(212) PRT

(213) E. Coli

(400) 161

Met Gln Val Leu Pro Pro Ser Ser Thr Gly Gly Pro Ser Arg Leu Phe
 1   5   10   15
Ile Met Asn Pro Val Ala Thr Thr Leu Leu Met Val Ala Ile Leu Leu
            20   25   30
Ala Gly Ile Ile Gly Tyr Arg Ala Leu Pro Val Ser Ala Leu Pro Gln
        35   40   45
Val Asp Tyr Pro Thr Ile Gln Val Val Thr Leu Tyr Pro Gly Ala Ser
    50   55   60
Pro Asp Val Met Thr Ser Ala Val Thr Ala Pro Leu Glu Arg Gln Phe
65   70   75   80
Gly Gln Met Ser Gly Leu Lys Gln Met Ser Ser Gln Ser Ser Leu Gly
                85   90   95
Ala Ser Val Ile Thr Leu Gln Phe Gln Leu Thr Leu Pro Leu Asp Val
            100   105   110
Ala Glu Gln Gln Val Gln Ala Ala Ile Asn Ala Ala Thr Asn Leu Leu
        115   120   125
Pro Ser Asp Leu Pro Asn Pro Pro Val Tyr Ser Lys Val Asn Pro Ala
    130   135   140
Asp Pro Pro Ile Met Thr Leu Ala Val Thr Ser Thr Ala Met Pro Met
145   150   155   160
Thr Gln Val Glu Asp Met Val Glu Thr Arg Val Ala Gln Lys Ile Ser
                165   170   175
```
```

Gln Ile Ser Gly Val Gly Leu Val Thr Leu Ser Gly Gly Gln Arg Pro
190 195 200
Ala Val Arg Val Lys Leu Asn Ala Gln Ala Ile Ala Ala Leu Gly Leu
205 210 215
Thr Ser Gln Thr Val Arg Thr Ala Ile Thr Gly Ala Asn Val Asn Ser
220 225 230
Ala Lys Gly Ser Leu Asp Gly Pro Ser Arg Ala Val Thr Leu Ser Ala
235 240 245
Asn Asp Gln Met Gln Ser Ala Glu Glu Tyr Arg Gln Leu Ile Ile Ala
250 255 260
Tyr Gln Asn Gly Ala Pro Ile Arg Leu Gly Asp Val Ala Thr Val Glu
265 270 275
Gln Gly Ala Glu Asn Ser Trp Leu Gly Ala Trp Ala Asn Lys Glu Gln
280 285 290
Ala Ile Val Met Asn Val Gln Arg Gln Pro Gly Ala Asn Ile Ile Ser
295 300 305
Thr Ala Asp Ser Ile Arg Gln Met Leu Pro Gln Leu Thr Glu Ser Leu
310 315 320
Pro Lys Ser Val Lys Val Thr Val Leu Ser Asp Arg Thr Thr Asn Ile
325 330 335
Arg Ala Ser Val Asp Asp Thr Gln Phe Glu Leu Met Met Ala Ile Ala
340 345 350
Leu Val Val Met Ile Ile Tyr Leu Phe Leu Arg Asn Ile Pro Ala Thr
355 360 365
Ile Ile Pro Gly Val Ala Val Pro Leu Ser Leu Ile Gly Thr Phe Ala
370 375 380
Val Met Val Phe Leu Asp Phe Ser Ile Asn Asn Leu Thr Leu Met Ala
385 390 395 400
Leu Thr Ile Ala Thr Gly Phe Val Val Asp Asp Ala Ile Val Val Ile
405 410 415
Glu Asn Ile Ser Arg Tyr Ile Glu Lys Gly Glu Lys Pro Leu Ala Ala
420 425 430
Ala Leu Lys Gly Ala Gly Glu Ile Gly Phe Thr Ile Ile Ser Leu Thr
435 440 445
Phe Ser Leu Ile Ala Val Leu Ile Pro Leu Leu Phe Met Gly Asp Ile
450 455 460
Val Gly Arg Leu Phe Arg Glu Phe Ala Ile Thr Leu Ala Val Ala Ile
465 470 475 480
Leu Ile Ser Ala Val Val Ser Leu Thr Leu Thr Pro Met Met Cys Ala
485 490 495
Arg Met Leu Ser Gln Glu Ser Leu Arg Lys Gln Asn Arg Phe Ser Arg
500 505 510
Ala Ser Glu Lys Met Phe Asp Arg Ile Ile Ala Ala Tyr Gly Arg Gly
515 520 525
Leu Ala Lys Val Leu Asn His Pro Trp Leu Thr Leu Ser Val Ala Leu
530 535 540
Ser Thr Leu Leu Leu Ser Val Leu Leu Trp Val Phe Ile Pro Lys Gly
545 550 555 560
Phe Phe Pro Val Gln Asp Asn Gly Ile Ile Gln Gly Thr Leu Gln Ala
565 570 575
Pro Gln Ser Ser Ser Phe Ala Asn Met Ala Gln Arg Gln Arg Gln Val
580 585 590
Ala Asp Val Ile Leu Gln Asp Pro Ala Val Gln Ser Leu Thr Ser Phe
595 600 605
Val Gly Val Asp Gly Thr Asn Pro Ser Leu Asn Ser Ala Arg Leu Gln
610 615 620
Ile Asn Leu Lys Pro Leu Asp Glu Arg Asp Asp Arg Val Gln Lys Val

625 630 635 640
Ile Ala Arg Leu Gln Thr Ala Val Asp Lys Val Pro Gly Val Asp Leu
645 650 655
Phe Leu Gln Pro Thr Gln Asp Leu Thr Ile Asp Thr Gln Val Ser Arg
660 665 670
Thr Gln Tyr Gln Phe Thr Leu Gln Ala Thr Ser Leu Asp Ala Leu Ser
675 680 685
Thr Trp Val Pro Gln Leu Met Glu Lys Leu Gln Gln Leu Pro Gln Leu
690 695 700
Ser Asp Val Ser Ser Asp Trp Gln Asp Lys Gly Leu Val Ala Tyr Val
705 710 715 720
Asn Val Asp Arg Asp Ser Ala Ser Arg Leu Gly Ile Ser Met Ala Asp
725 730 735
Val Asp Asn Ala Leu Tyr Asn Ala Phe Gly Gln Arg Leu Ile Ser Thr
740 745 750
Ile Tyr Thr Gln Ala Asn Gln Tyr Arg Val Val Leu Glu His Asn Thr
755 760 765
Glu Asn Thr Pro Gly Leu Ala Ala Leu Asp Thr Ile Arg Leu Thr Ser
770 775 780
Ser Asp Gly Gly Val Val Pro Leu Ser Ser Ile Ala Lys Ile Glu Gln
785 790 795 800
Arg Phe Ala Pro Leu Ser Ile Asn His Leu Asp Gln Phe Pro Val Thr
805 810 815
Thr Ile Ser Phe Asn Val Pro Asp Asn Tyr Ser Leu Gly Asp Ala Val
820 825 830
Gln Ala Ile Met Asp Thr Glu Lys Thr Leu Asn Leu Pro Val Asp Ile
835 840 845
Thr Thr Gln Phe Gln Gly Ser Thr Leu Ala Phe Gln Ser Ala Leu Gly
850 855 860
Ser Thr Val Trp Leu Ile Val Ala Ala Val Val Ala Met Tyr Ile Val
865 870 875 880
Leu Gly Ile Leu Tyr Glu Ser Phe Ile His Pro Ile Thr Ile Leu Ser
885 890 895
Thr Leu Pro Thr Ala Gly Val Gly Ala Leu Leu Ala Leu Leu Ile Ala
900 905 910
Gly Ser Glu Leu Asp Val Ile Ala Ile Ile Gly Ile Ile Leu Leu Ile
915 920 925
Gly Ile Val Lys Lys Asn Ala Ile Met Met Ile Asp Phe Ala Leu Ala
930 935 940
Ala Gln Arg Glu Gln Gly Met Ser Pro Arg Glu Ala Ile Tyr Gln Ala
945 950 955 960
Cys Leu Leu Arg Phe Arg Pro Ile Leu Met Thr Thr Leu Ala Ala Leu
965 970 975
Leu Gly Ala Leu Pro Leu Met Leu Ser Thr Gly Val Gly Ala Glu Leu
980 985 990
Arg Arg Pro Leu Gly Ile Gly Met Val Gly Gly Leu Ile Val Ser Gln
995 1000 1005
Val Leu Thr Leu Phe Thr Thr Pro Val Ile Tyr Leu Leu Phe Asp Arg
1010 1015 1020
Leu Ala Leu Trp Thr Lys Ser Arg Phe Ala Arg His Glu Glu Glu Ala
1025 1030 1035 1040

<210> 253
<211> 1025
<212> PRT
<213> E. Coli

<400> 383

Met Lys Phe Phe Ala Leu Phe Ile Tyr Arg Pro Val Ala Thr Ile Leu
1 5 10 15

Leu Ser Val Ala Ile Thr Leu Cys Gly Ile Leu Gly Phe Arg Met Leu
20 25 30

Pro Val Ala Pro Leu Pro Gln Val Asp Phe Pro Val Ile Ile Val Ser
35 40 45

Ala Ser Leu Pro Gly Ala Ser Pro Glu Thr Met Ala Ser Ser Val Ala
50 55 60

Thr Pro Leu Glu Arg Ser Leu Gly Arg Ile Ala Gly Val Ser Glu Met
65 70 75 80

Thr Ser Ser Ser Ser Leu Gly Ser Thr Arg Ile Ile Leu Gln Phe Asp
85 90 95

Phe Asp Arg Asp Ile Asn Gly Ala Ala Arg Asp Val Gln Ala Ala Ile
100 105 110

Asn Ala Ala Gln Ser Leu Leu Pro Ser Gly Met Pro Ser Arg Pro Thr
115 120 125

Tyr Arg Lys Ala Asn Pro Ser Asp Ala Pro Ile Met Ile Leu Thr Leu
130 135 140

Thr Ser Asp Thr Tyr Ser Gln Gly Glu Leu Tyr Asp Phe Ala Ser Thr
145 150 155 160

Gln Leu Ala Pro Thr Ile Ser Gln Ile Asp Gly Val Gly Asp Val Asp
165 170 175

Val Gly Gly Ser Ser Leu Pro Ala Val Arg Val Gly Leu Asn Pro Gln
180 185 190

Ala Leu Phe Asn Gln Gly Val Ser Leu Asp Asp Val Arg Thr Ala Val
195 200 205

Ser Asn Ala Asn Val Arg Lys Pro Gln Gly Ala Leu Gln Asp Gly Thr
210 215 220

His Asn Trp Gln Ile Gln Thr Asn Asp Glu Leu Lys Thr Ala Ala Glu
225 230 235 240

Tyr Gln Pro Leu Ile Ile His Tyr Asn Asn Gly Gly Ala Val Arg Leu
245 250 255

Gly Asp Val Ala Thr Val Thr Asp Ser Val Gln Asp Val Arg Asn Ala
260 265 270

Gly Met Thr Asn Ala Lys Pro Ala Ile Leu Leu Met Ile Arg Lys Leu
275 280 285

Pro Gln Ala Asn Ile Ile Gln Thr Val Asp Ser Ile Arg Ala Lys Leu
290 295 300

Pro Gln Leu Gln Glu Thr Ile Pro Ala Ala Ile Asp Leu Gln Ile Ala
305 310 315 320

Gln Asp Arg Ser Pro Ile Thr Ile Arg Ala Ser Leu Glu Glu Val Glu Gln
325 330 335

Thr Leu Ile Ile Ser Val Ala Leu Val Ile Leu Val Val Phe Leu Phe
340 345 350

Leu Arg Ser Gly Arg Ala Thr Ile Ile Pro Ala Val Ser Val Pro Val
355 360 365

Ser Leu Ile Gly Thr Phe Ala Ala Met Tyr Leu Cys Gly Phe Ser Leu
370 375 380

Asn Asn Leu Ser Leu Met Ala Leu Thr Ile Ala Thr Gly Phe Val Val
385 390 395 400

Asp Asp Ala Ile Val Val Leu Glu Asn Ile Ala Arg His Leu Glu Ala
405 410 415

Gly Met Lys Pro Leu Gln Ala Ala Leu Gln Gly Thr Arg Glu Val Gly
420 425 430

Phe Thr Val Leu Ser Met Ser Leu Ser Leu Val Ala Val Phe Leu Pro

```
                    435                 440                 445
Leu Leu Leu Met Gly Gly Leu Pro Gly Arg Leu Leu Arg Glu Phe Ala
        450                 455                 460
Val Thr Leu Ser Val Ala Ile Gly Ile Ser Leu Leu Val Ser Leu Thr
465                 470                 475                 480
Leu Thr Pro Met Met Cys Gly Trp Met Leu Lys Ala Ser Lys Pro Arg
                485                 490                 495
Glu Gln Lys Arg Leu Arg Gly Phe Gly Arg Met Leu Val Ala Leu Gln
            500                 505                 510
Gln Gly Tyr Gly Lys Ser Leu Lys Trp Val Leu Asn His Thr Arg Leu
        515                 520                 525
Val Gly Val Val Leu Leu Gly Thr Ile Ala Leu Asn Ile Trp Leu Tyr
    530                 535                 540
Ile Ser Ile Pro Lys Thr Phe Phe Pro Glu Gln Asp Thr Gly Val Leu
545                 550                 555                 560
Met Gly Gly Ile Gln Ala Asp Gln Ser Ile Ser Phe Gln Ala Met Arg
                565                 570                 575
Gly Lys Leu Gln Asp Phe Met Lys Ile Ile Arg Asp Asp Pro Ala Val
            580                 585                 590
Asp Asn Val Thr Gly Phe Thr Gly Gly Ser Arg Val Asn Ser Gly Met
        595                 600                 605
Met Pro Ile Thr Leu Lys Pro Arg Asp Glu Arg Ser Gln Thr Ala Gln
    610                 615                 620
Gln Ile Ile Asp Arg Leu Arg Val Lys Leu Ala Lys Gln Pro Gly Ala
625                 630                 635                 640
Asn Leu Phe Leu Met Ala Val Gln Asp Ile Arg Val Gly Gly Arg Gln
                645                 650                 655
Ser Asn Ala Ser Tyr Gln Tyr Thr Leu Leu Ser Asp Asp Leu Ala Ala
            660                 665                 670
Leu Arg Glu Trp Glu Pro Lys Ile Arg Lys Lys Leu Ala Thr Leu Pro
        675                 680                 685
Glu Leu Ala Asp Val Asn Ser Asp Gln Gln Asp Asn Gly Ala Glu Met
    690                 695                 700
Asn Leu Val Tyr Asp Arg Asp Thr Met Ala Arg Leu Gly Ile Asp Val
705                 710                 715                 720
Gln Ala Ala Asn Ser Leu Leu Asn Asn Ala Phe Gly Gln Arg Gln Ile
                725                 730                 735
Ser Thr Ile Tyr Gln Pro Met Asn Gln Tyr Lys Val Val Met Glu Val
            740                 745                 750
Asp Pro Arg Tyr Thr Gln Asp Ile Ser Ala Leu Glu Lys Met Phe Val
        755                 760                 765
Ile Asn Asn Glu Gly Lys Ala Ile Pro Leu Ser Tyr Phe Ala Lys Trp
    770                 775                 780
Gln Pro Ala Asn Ala Pro Leu Ser Val Asn His Gln Gly Leu Ser Ala
785                 790                 795                 800
Ala Ser Thr Ile Ser Phe Asn Leu Pro Thr Gly Lys Ser Leu Ser Asp
                805                 810                 815
Ala Ser Ala Ala Ile Asp Arg Ala Met Thr Gln Leu Gly Val Pro Ser
            820                 825                 830
Thr Val Arg Gly Ser Phe Ala Gly Thr Ala Gln Val Phe Gln Glu Thr
        835                 840                 845
Met Asn Ser Gln Val Ile Leu Ile Ile Ala Ala Ile Ala Thr Val Tyr
    850                 855                 860
Ile Val Leu Gly Ile Leu Tyr Gln Ser Tyr Val His Pro Leu Thr Ile
865                 870                 875                 880
Leu Ser Thr Leu Pro Ser Ala Gly Val Gly Ala Leu Leu Ala Leu Glu
                885                 890                 895
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Leu Phe Asn Ala Pro Phe Ser Leu Ile Ala Leu Ile Gly Ile Met Leu
900 905 910
Leu Ile Gly Ile Val Lys Lys Asn Ala Ile Met Met Val Asp Phe Ala
915 920 925
Leu Glu Ala Gln Arg His Gly Asn Leu Thr Pro Gln Glu Ala Ile Phe
930 935 940
Gln Ala Cys Leu Leu Arg Phe Arg Pro Ile Met Met Thr Thr Leu Ala
945 950 955 960
Ala Leu Phe Gly Ala Leu Pro Leu Val Leu Ser Gly Gly Asp Gly Ser
965 970 975
Glu Leu Arg Gln Pro Leu Gly Ile Thr Ile Val Gly Gly Leu Val Met
980 985 990
Ser Gln Leu Leu Thr Leu Tyr Thr Thr Pro Val Val Tyr Leu Phe Phe
995 1000 1005
Asp Arg Leu Arg Leu Arg Phe Ser Arg Lys Pro Lys Gln Thr Val Thr
1010 1015 1020
Glu
1025

<200> 384
<211> 471
<212> PRT
<213> E. Coli

<400> 384
Met Thr Asp Leu Pro Asp Ser Thr Arg Trp Gln Leu Trp Ile Val Ala
1 5 10 15
Phe Gly Phe Phe Met Gln Ser Leu Asp Thr Thr Ile Val Asn Thr Ala
20 25 30
Leu Pro Ser Met Ala Gln Ser Leu Gly Glu Ser Pro Leu His Met His
35 40 45
Met Val Ile Val Ser Tyr Val Leu Thr Val Ala Val Met Leu Pro Ala
50 55 60
Ser Gly Trp Leu Ala Asp Lys Val Gly Val Arg Asn Ile Phe Phe Thr
65 70 75 80
Ala Ile Val Leu Phe Thr Leu Gly Ser Leu Phe Cys Ala Leu Ser Gly
85 90 95
Thr Leu Asn Gln Leu Leu Leu Ala Arg Ala Leu Gln Gly Val Gly Gly
100 105 110
Ala Met Met Val Pro Val Gly Arg Leu Thr Val Met Lys Ile Val Pro
115 120 125
Arg Glu Gln Tyr Met Ala Ala Met Thr Phe Val Thr Leu Pro Gly Gln
130 135 140
Val Gly Pro Leu Leu Gly Pro Ala Leu Gly Gly Leu Leu Val Glu Tyr
145 150 155 160
Ala Ser Trp His Trp Ile Phe Leu Ile Asn Ile Pro Val Gly Ile Ile
165 170 175
Gly Ala Ile Ala Thr Leu Leu Leu Met Pro Asn Tyr Thr Met Gln Thr
180 185 190
Arg Arg Phe Asp Leu Ser Gly Phe Leu Leu Leu Ala Val Gly Met Ala
195 200 205
Val Leu Thr Leu Ala Leu Asp Gly Ser Lys Gly Thr Gly Leu Ser Pro
210 215 220
Leu Thr Ile Ala Gly Leu Val Ala Val Gly Val Val Ala Leu Val Leu
225 230 235 240
Tyr Leu Leu His Ala Arg Asn Asn Asn Arg Ala Leu Phe Ser Leu Lys

245 250 255

Leu Phe Arg Thr Arg Thr Phe Ser Leu Gly Leu Ala Gly Ser Phe Ala
260 265 270

Gly Arg Ile Gly Ser Gly Met Leu Pro Phe Met Thr Pro Val Phe Leu
275 280 285

Gln Ile Gly Leu Gly Phe Ser Pro Phe His Ala Gly Leu Met Met Ile
290 295 300

Pro Met Val Leu Gly Ser Met Gly Met Lys Arg Ile Val Val Gln Val
305 310 315 320

Val Asn Arg Phe Gly Tyr Arg Arg Val Leu Val Ala Thr Thr Leu Gly
325 330 335

Leu Ser Leu Val Thr Leu Leu Phe Met Thr Thr Ala Leu Leu Gly Trp
340 345 350

Tyr Tyr Val Leu Pro Phe Val Leu Phe Leu Gln Gly Met Val Asn Ser
355 360 365

Thr Arg Phe Ser Ser Met Asn Thr Leu Thr Leu Lys Asp Leu Pro Asp
370 375 380

Asn Leu Ala Ser Ser Gly Asn Ser Leu Leu Ser Met Ile Met Gln Leu
385 390 395 400

Ser Met Ser Ile Gly Val Thr Ile Ala Gly Leu Leu Leu Gly Leu Phe
405 410 415

Gly Ser Gln His Val Ser Val Asp Ser Gly Thr Thr Gln Thr Val Phe
420 425 430

Met Tyr Thr Trp Leu Ser Met Ala Leu Ile Ile Ala Leu Pro Ala Phe
435 440 445

Ile Phe Ala Arg Val Pro Asn Asp Thr His Gln Asn Val Ala Ile Ser
450 455 460

Arg Arg Lys Arg Ser Ala Gln
465 470

<210> 165
<211> 144
<212> PRT
<213> E. Coli

<400> 165

Met Glu Ile Arg Ile Met Leu Phe Ile Leu Met Met Met Val Met Pro
1 5 10 15

Val Ser Tyr Ala Ala Cys Tyr Ser Glu Leu Ser Val Gln His Asn Leu
20 25 30

Val Val Gln Gly Asp Phe Ala Leu Thr Gln Thr Gln Met Ala Thr Tyr
35 40 45

Glu His Asn Phe Asn Asp Ser Ser Cys Val Ser Thr Asn Thr Ile Thr
50 55 60

Pro Met Ser Pro Ser Asp Ile Ile Val Gly Leu Tyr Asn Asp Thr Ile
65 70 75 80

Lys Leu Asn Leu His Phe Glu Trp Thr Asn Lys Asn Asn Ile Thr Leu
85 90 95

Ser Asn Asn Gln Thr Ser Phe Thr Ser Gly Tyr Ser Val Thr Val Thr
100 105 110

Pro Ala Ala Ser Asn Ala Lys Val Asn Val Ser Ala Gly Gly Gly Gly
115 120 125

Ser Val Met Ile Asn Gly Val Ala Thr Leu Ser Ser Ala Ser Ser Ser
130 135 140

Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly
145 150 155 160

Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln
165 170 175
Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile
180 185 190
Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile
195 200 205
Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser
210 215 220
Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln
225 230 235 240
Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu
245 250 255
Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val
260 265 270
Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile
275 280 285
Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys
290 295 300
Ser Lys Leu Thr Asp Thr Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr
305 310 315 320
Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr
325 330 335
Ala Leu Ile Asn Val Lys Tyr Asp
340

<210> 196
<211> 26
<212> PRT
<213> E. Coli

<400> 196
Met Leu Arg Met Thr Pro Leu Ala Ser Ala Ile Val Ala Leu Leu Leu
1 5 10 15
Gly Ile Glu Ala Tyr Ala Ala Glu Glu Thr Phe Asp Thr His Phe Met
20 25 30
Ile Gly Gly Met Lys Asp Gln Gln Val Ala Asn Ile Arg Leu Asp Asp
35 40 45
Asn Gln Pro Leu Pro Gly Gln Tyr Asp Ile Asp Ile Tyr Val Asn Lys
50 55 60
Gln Trp Arg Gly Lys Tyr Glu Ile Ile Val Lys Asp Asn Pro Gln Glu
65 70 75 80
Thr Cys Leu Ser Arg Gln Val Ile Lys Arg Leu Gly Ile Asn Ser Asp
85 90 95
Asn Phe Ala Ser Gly Lys Gln Cys Leu Thr Phe Glu Gln Leu Val Gln
100 105 110
Gly Gly Ser Tyr Thr Trp Asp Ile Gly Val Phe Arg Leu Asp Phe Ser
115 120 125
Val Pro Gln Ala Trp Val Glu Glu Leu Glu Ser Gly Tyr Val Pro Pro
130 135 140
Glu Asn Trp Gln Arg Gly Ile Asn Ala Phe Tyr Thr Ser Tyr Tyr Leu
145 150 155 160
Ser Gln Tyr Tyr Ser Asp Tyr Lys Ala Ser Gly Asn Asn Lys Ser Thr
165 170 175
Tyr Val Arg Phe Asn Ser Gly Leu Asn Leu Leu Gly Trp Gln Leu His
180 185 190
Ser Asp Ala Ser Phe Ser Lys Thr Asn Asn Asn Pro Gly Val Trp Lys

Ser Asn Thr Leu Tyr Leu Glu Arg Gly Phe Ala Gln Leu Leu Gly Thr
Leu Arg Val Gly Asp Met Tyr Thr Ser Ser Asp Ile Phe Asp Ser Val
Arg Phe Arg Gly Val Arg Leu Phe Arg Asp Met Gln Met Leu Pro Asn
Ser Lys Gln Asn Phe Thr Pro Arg Val Gln Gly Ile Ala Gln Ser Asn
Ala Leu Val Thr Ile Glu Gln Asn Gly Phe Val Val Tyr Gln Lys Glu
Val Pro Pro Gly Pro Phe Ala Ile Thr Asp Leu Gln Leu Ala Gly Gly
Gly Ala Asp Leu Asp Val Ser Val Lys Glu Ala Asp Gly Ser Val Thr
Thr Tyr Leu Val Pro Tyr Ala Ala Val Pro Asn Met Leu Gln Pro Gly
Val Ser Lys Tyr Asp Leu Ala Ala Gly Arg Ser His Ile Glu Gly Ala
Ser Lys Gln Ser Asp Phe Val Gln Ala Gly Tyr Gln Tyr Gly Phe Asn
Asn Leu Leu Thr Leu Tyr Gly Gly Ser Met Val Ala Asn Asn Tyr Tyr
Ala Phe Thr Leu Gly Ala Gly Trp Asn Thr Arg Ile Gly Ala Ile Ser
Val Asp Ala Thr Lys Ser His Ser Lys Gln Asp Asn Gly Asp Val Phe
Asp Gly Gln Ser Tyr Gln Ile Ala Tyr Asn Lys Phe Val Ser Gln Thr
Ser Thr Arg Phe Gly Leu Ala Ala Trp Arg Tyr Ser Ser Arg Asp Tyr
Arg Thr Phe Asn Asp His Val Trp Ala Asn Asn Lys Asp Asn Tyr Arg
Arg Asp Glu Asn Asp Val Tyr Asp Ile Ala Asp Tyr Tyr Gln Asn Asp
Phe Gly Arg Lys Asn Ser Phe Ser Ala Asn Met Ser Gln Ser Leu Pro
Glu Gly Trp Gly Ser Val Ser Leu Ser Thr Leu Trp Arg Asp Tyr Trp
Gly Arg Ser Gly Ser Ser Lys Asp Tyr Gln Leu Ser Tyr Ser Asn Asn
Leu Arg Arg Ile Ser Tyr Thr Leu Ala Ala Ser Gln Ala Tyr Asp Glu
Asn His His Gln Glu Lys Arg Phe Asn Ile Phe Ile Ser Ile Pro Phe
Asp Trp Gly Asp Asp Val Ser Thr Pro Arg Arg Gln Ile Tyr Met Ser
Asn Ser Thr Thr Phe Asp Asp Gln Gly Phe Ala Ser Asn Asn Thr Gly
Leu Ser Gly Thr Val Gly Ser Arg Asp Gln Phe Asn Tyr Gly Val Asn
Leu Ser His Gln His Gln Gly Asn Glu Thr Thr Ala Gly Ala Asn Leu
Thr Trp Asn Ala Pro Val Ala Thr Val Asn Gly Ser Tyr Ser Gln Ser
Ser Thr Tyr Arg Gln Ala Gly Ala Ser Val Ser Gly Gly Ile Val Ala

Trp Ser Gly Gly Val Asn Leu Ala Asn Arg Leu Ser Glu Thr Phe Ala
660 665 670
Val Met Asn Ala Pro Gly Ile Lys Asp Ala Tyr Val Asn Gly Gln Lys
675 680 685
Tyr Arg Thr Thr Asn Arg Asn Gly Val Val Ile Tyr Asp Gly Met Thr
690 695 700
Pro Tyr Arg Glu Asn His Leu Met Leu Asp Val Ser Gln Ser Asp Ser
705 710 715 720
Glu Ala Glu Leu Arg Gly Asn Arg Lys Ile Ala Ala Pro Tyr Arg Gly
725 730 735
Ala Val Val Leu Val Asn Phe Asp Thr Asp Gln Arg Lys Pro Trp Phe
740 745 750
Ile Lys Ala Leu Arg Ala Asp Gly Gln Ser Leu Thr Phe Gly Tyr Glu
755 760 765
Val Asn Asp Ile His Gly His Asn Ile Gly Val Val Gly Gln Gly Ser
770 775 780
Gln Leu Pro Ile Arg Thr Asn Glu Val Pro Pro Ser Val Asn Val Ala
785 790 795 800
Ile Asp Lys Gln Gln Gly Leu Ser Cys Thr Ile Thr Phe Gly Lys Glu
805 810 815
Ile Asp Gln Ser Arg Asn Tyr Ile Cys Gln
820 825

<211> 837
<212> DNA
<213> E. Coli

<400> 67
Met Ala Asn Ile Pro Trp Arg Pro Phe Asn Leu Arg Gly Ile Lys Met
1 5 10 15
Lys Gly Leu Leu Ser Leu Leu Ile Phe Ser Met Val Leu Pro Ala His
20 25 30
Ala Gly Leu Val Ile Tyr Gly Thr Arg Ile Ile Tyr Pro Ala Glu Asn
35 40 45
Lys Glu Val Met Val Gln Leu Met Asn Gln Gly Asn Arg Ser Ser Leu
50 55 60
Leu Gln Ala Trp Ile Asp Asp Gly Asp Thr Ser Leu Pro Pro Glu Lys
65 70 75 80
Ile Gln Val Pro Phe Met Leu Thr Pro Pro Val Ala Lys Ile Gly Ala
85 90 95
Asn Ser Gly Gln Gln Val Lys Ile Lys Ile Met Pro Asn Lys Leu Pro
100 105 110
Thr Asp Arg Glu Ser Ile Phe Tyr Leu Asn Val Leu Asp Ile Pro Pro
115 120 125
Asn Ser Pro Glu Gln Glu Gly Lys Asn Ala Leu Lys Phe Ala Met Gln
130 135 140
Asn Arg Ile Lys Leu Phe Tyr Arg Pro Ala Gly Ile Ala Pro Val Asn
145 150 155 160
Lys Ala Thr Phe Lys Lys Leu Leu Val Asn Arg Ser Gly Asn Gly Leu
165 170 175
Val Ile Lys Asn Asp Ser Ala Asn Trp Val Thr Ile Ser Asp Val Lys
180 185 190
Ala Asn Asn Val Lys Val Asn Tyr Glu Thr Ile Met Ile Ala Pro Leu
195 200 205
Glu Ser Gln Ser Val Asn Val Lys Ser Asn Asn Ala Asn Asn Trp His

210 215 220

Leu Thr Ile Ile Asp Asp His Gly Asn Tyr Ile Ser Asp Lys Ile
225 230 235

(210) 185
(211) 180
(212) PRT
(213) E. Coli

(400) 185

Met Lys Arg Ser Ile Ile Ala Ala Ala Val Phe Ser Ser Phe Phe Met
1 5 10 15
Ser Ala Gly Val Phe Ala Ala Asp Val Asp Thr Gly Thr Leu Thr Ile
20 25 30
Lys Gly Asn Ile Ala Glu Ser Pro Cys Lys Phe Glu Ala Gly Gly Asp
35 40 45
Ser Val Ser Ile Asn Met Pro Thr Val Pro Thr Ser Val Phe Glu Gly
50 55 60
Lys Ala Lys Tyr Ser Thr Tyr Asp Asp Ala Val Gly Val Thr Ser Ser
65 70 75 80
Met Leu Lys Ile Ser Cys Pro Lys Glu Val Ala Gly Val Lys Leu Ser
85 90 95
Leu Ile Thr Asn Asp Lys Ile Thr Gly Asn Asp Lys Ala Ile Ala Ser
100 105 110
Ser Asn Asp Thr Val Gly Tyr Tyr Leu Tyr Leu Gly Asp Asn Ser Asp
115 120 125
Val Leu Asp Val Ser Ala Pro Phe Asn Ile Glu Ser Tyr Lys Thr Ala
130 135 140
Glu Gly Gln Tyr Ala Ile Pro Phe Lys Ala Lys Tyr Leu Lys Leu Thr
145 150 155 160
Asp Asn Ser Val Gln Ser Gly Asp Val Leu Ser Ser Leu Val Met Arg
165 170 175
Val Ala Gln Asp
180

(210) 186
(211) 112
(212) PRT
(213) E. Coli

(400) 186

Met Ser Ser Glu Arg Asp Leu Val Asn Phe Leu Gly Asp Phe Ser Met
1 5 10 15
Asp Val Ala Lys Ala Val Ile Ala Gly Gly Val Ala Thr Ala Ile Gly
20 25 30
Ser Leu Ala Ser Phe Ala Cys Val Ser Phe Gly Pro Pro Val Ile Leu
35 40 45
Val Gly Gly Ala Ile Leu Leu Thr Gly Ile Val Tyr Thr Val Val Leu
50 55 60
Asn Gln Ile Asp Ala Gln Cys His Leu Ser Glu Lys Leu Lys Tyr Ala
65 70 75 80
Ile Arg Asp Gly Leu Lys Arg Gln Gln Glu Leu Asp Lys Trp Lys Arg
85 90 95
Glu Asn Met Thr Pro Phe Met Tyr Val Leu Asn Thr Pro Pro Val Ile

100 105 110

(210) 140
(211) 149
(212) PRT
(213) E. Coli

(400) 140

Met Thr Asp Tyr Leu Leu Leu Phe Val Gly Thr Val Leu Val Asn Asn
1 5 10 15
Phe Val Leu Val Lys Phe Leu Gly Leu Cys Pro Phe Met Gly Val Ser
20 25 30
Lys Lys Leu Glu Thr Ala Met Gly Met Gly Leu Ala Thr Thr Phe Val
35 40 45
Met Thr Leu Ala Ser Ile Cys Ala Trp Leu Ile Asp Thr Trp Ile Leu
50 55 60
Ile Pro Leu Asn Leu Ile Tyr Leu Arg Thr Leu Ala Phe Ile Leu Val
65 70 75 80
Ile Ala Val Val Val Gln Phe Thr Glu Met Val Val Arg Lys Thr Ser
85 90 95
Pro Val Leu Tyr Arg Leu Leu Gly Ile Phe Leu Pro Leu Ile Thr Thr
100 105 110
Asn Cys Ala Val Leu Gly Val Ala Leu Leu Asn Ile Asn Leu Gly His
115 120 125
Asn Phe Leu Gln Ser Ala Leu Tyr Gly Phe Ser Ala Ala Val Gly Phe
130 135 140
Ser Leu Val Met Val Leu Phe Ala Ala Ile Arg Glu Arg Leu Ala Val
145 150 155 160
Ala Asp Val Pro Ala Pro Phe Arg Gly Asn Ala Ile Ala Leu Ile Thr
165 170 175
Ala Gly Leu Met Ser Leu Ala Phe Met Gly Phe Ser Gly Leu Val Lys
180 185 190
Leu

(210) 141
(211) 142
(212) PRT
(213) E. Coli

(400) 141

Met Asn Ala Ile Trp Ile Ala Val Ala Ala Val Ser Leu Leu Gly Leu
1 5 10 15
Ala Phe Gly Ala Ile Leu Gly Tyr Ala Ser Arg Arg Phe Ala Val Glu
20 25 30
Asp Asp Pro Val Val Glu Lys Ile Asp Glu Ile Leu Pro Gln Ser Gln
35 40 45
Cys Gly Gln Cys Gly Tyr Pro Gly Cys Arg Pro Tyr Ala Glu Ala Ile
50 55 60
Ser Cys Asn Gly Glu Lys Ile Asn Arg Cys Ala Pro Gly Gly Glu Ala
65 70 75 80
Val Met Leu Lys Ile Ala Glu Leu Leu Asn Val Glu Pro Gln Pro Leu
85 90 95
Asp Gly Glu Ala Gln Glu Ile Thr Pro Ala Arg Met Val Ala Val Ile

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                100                 105                 110
Asp Glu Asn Asn Cys Ile Gly Cys Thr Lys Cys Ile Gln Ala Cys Pro
            115                 120                 125
Val Asp Ala Ile Val Gly Ala Thr Arg Ala Met His Thr Val Met Ser
        130                 135                 140
Asp Leu Cys Thr Gly Cys Asn Leu Cys Val Asp Pro Cys Pro Thr His
145                 150                 155                 160
Cys Ile Ser Leu Gln Pro Val Ala Glu Thr Pro Asp Ser Trp Lys Trp
                165                 170                 175
Asp Leu Asn Thr Ile Pro Val Arg Ile Ile Pro Val Glu His His Ala
            180                 185                 190
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<210> 230
<211> 740
<212> PRT
<213> E. Coli

<400> 137


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Met Leu Lys Leu Phe Ser Ala Phe Arg Lys Asn Lys Ile Trp Asp Phe
 1               5                  10                  15
Asn Gly Gly Ile His Pro Pro Glu Met Lys Thr Gln Ser Asn Gly Thr
            20                  25                  30
Pro Leu Arg Gln Val Pro Leu Ala Gln Arg Phe Val Ile Pro Leu Lys
        35                  40                  45
Gln His Ile Gly Ala Glu Gly Glu Leu Cys Val Ser Val Gly Asp Lys
    50                  55                  60
Val Leu Arg Gly Gln Pro Leu Thr Arg Gly Arg Gly Lys Met Leu Pro
65                  70                  75                  80
Val His Ala Pro Thr Ser Gly Thr Val Thr Ala Ile Ala Pro His Ser
                85                  90                  95
Thr Ala His Pro Ser Ala Leu Ala Glu Leu Ser Val Ile Ile Asp Ala
            100                 105                 110
Asp Gly Glu Asp Cys Trp Ile Pro Arg Asp Gly Trp Ala Asp Tyr Arg
        115                 120                 125
Thr Arg Ser Arg Glu Glu Leu Ile Glu Arg Ile His Gln Phe Gly Val
    130                 135                 140
Ala Gly Leu Gly Gly Ala Gly Phe Pro Thr Gly Val Lys Leu Gln Gly
145                 150                 155                 160
Gly Gly Asp Lys Ile Glu Thr Leu Ile Ile Asn Ala Ala Glu Cys Glu
                165                 170                 175
Pro Tyr Ile Thr Ala Asp Asp Arg Leu Met Gln Asp Cys Ala Ala Gln
            180                 185                 190
Val Val Glu Gly Ile Arg Ile Leu Ala His Ile Leu Gln Pro Arg Glu
        195                 200                 205
Ile Leu Ile Gly Ile Glu Asp Asn Lys Pro Gln Ala Ile Ser Met Leu
    210                 215                 220
Arg Ala Val Leu Ala Asp Ser Asn Asp Ile Ser Leu Arg Val Ile Pro
225                 230                 235                 240
Thr Lys Tyr Pro Ser Gly Gly Ala Lys Gln Leu Thr Tyr Ile Leu Thr
                245                 250                 255
Gly Lys Gln Val Pro His Gly Gly Arg Ser Ser Asp Ile Gly Val Leu
            260                 265                 270
Met Gln Asn Val Gly Thr Ala Tyr Ala Val Lys Arg Ala Val Ile Asp
        275                 280                 285
Gly Gln Pro Ile Thr Glu Arg Val Val Thr Leu Thr Gly Glu Ala Ile
    290                 295                 300
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Ala Arg Pro Gly Asn Val Trp Ala Arg Leu Gly Thr Pro Val Arg His
305 310 315 320
Leu Leu Asn Asp Ala Gly Phe Cys Pro Ser Ala Asp Gln Met Val Ile
325 330 335
Met Gly Gly Pro Leu Met Gly Phe Thr Leu Pro Trp Leu Asp Val Pro
340 345 350
Val Val Lys Ile Thr Asn Cys Leu Leu Ala Pro Ser Ala Asn Glu Leu
355 360 365
Gly Glu Pro Gln Glu Glu Gln Ser Cys Ile Arg Cys Ser Ala Cys Ala
370 375 380
Asp Ala Cys Pro Ala Asp Leu Leu Pro Gln Gln Leu Tyr Trp Phe Ser
385 390 395 400
Lys Gly Gln Gln His Asp Lys Ala Thr Thr His Asn Ile Ala Asp Cys
405 410 415
Ile Gln Cys Gly Ala Cys Ala Trp Val Cys Pro Ser Asn Ile Pro Leu
420 425 430
Val Gln Tyr Phe Arg Gln Glu Lys Ala Glu Ile Ala Ala Ile Arg Gln
435 440 445
Glu Glu Lys Arg Ala Ala Glu Ala Lys Ala Arg Phe Glu Ala Arg Gln
450 455 460
Ala Arg Leu Glu Arg Glu Lys Ala Ala Arg Leu Glu Arg His Lys Ser
465 470 475 480
Ala Ala Val Gln Pro Ala Ala Lys Asp Lys Asp Ala Ile Ala Ala Ala
485 490 495
Leu Ala Arg Val Lys Glu Lys Gln Ala Gln Ala Thr Gln Pro Ile Val
500 505 510
Ile Lys Ala Gly Glu Arg Pro Asp Asn Ser Ala Ile Ile Ala Ala Arg
515 520 525
Glu Ala Arg Lys Ala Gln Ala Arg Ala Lys Gln Ala Glu Leu Gln Gln
530 535 540
Thr Asn Asp Ala Ala Thr Val Ala Asp Pro Arg Lys Thr Ala Val Glu
545 550 555 560
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
565 570 575
Asn Ala Glu Pro Glu Gln Gln Val Asp Pro Arg Lys Ala Ala Val Glu
580 585 590
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
595 600 605
Asn Ala Glu Pro Glu Gln Gln Val Asp Pro Arg Lys Ala Ala Val Glu
610 615 620
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
625 630 635 640
Asn Ala Glu Pro Glu Gln Gln Val Asp Pro Arg Lys Ala Ala Val Glu
645 650 655
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Arg Glu Gln Gln Pro Ala
660 665 670
Asn Ala Glu Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Glu
675 680 685
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
690 695 700
Asn Ala Val Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Ala
705 710 715 720
Ala Ala Ile Ala Arg Ala Gln Ala Lys Lys Ala Ala Gln Gln Lys Val
725 730 735
Val Asn Glu Asp
740

<210> 193
<211> 342
<212> PRT
<213> E. Coli

<400> 193

Met	Val	Phe	Arg	Ile	Ala	Ser	Ser	Pro	Tyr	Thr	His	Asn	Gln	Arg	Gln
1				5					10					15	
Thr	Ser	Arg	Ile	Met	Leu	Leu	Val	Leu	Leu	Ala	Ala	Val	Pro	Gly	Ile
			20					25					30		
Ala	Ala	Gln	Leu	Trp	Phe	Phe	Gly	Trp	Gly	Thr	Leu	Val	Gln	Ile	Leu
		35					40					45			
Leu	Ala	Ser	Val	Ser	Ala	Leu	Leu	Ala	Glu	Ala	Leu	Val	Leu	Lys	Leu
	50					55					60				
Arg	Lys	Gln	Ser	Val	Ala	Ala	Thr	Leu	Lys	Asp	Asn	Ser	Ala	Leu	Leu
65					70					75					80
Thr	Gly	Leu	Leu	Leu	Ala	Val	Ser	Ile	Pro	Pro	Leu	Ala	Pro	Trp	Trp
				85					90					95	
Met	Val	Val	Leu	Gly	Thr	Val	Phe	Ala	Val	Ile	Ile	Ala	Lys	Gln	Leu
			100					105					110		
Tyr	Gly	Gly	Leu	Gly	Gln	Asn	Pro	Phe	Asn	Pro	Ala	Met	Ile	Gly	Tyr
		115					120					125			
Val	Val	Leu	Leu	Ile	Ser	Phe	Pro	Val	Gln	Met	Thr	Ser	Trp	Leu	Pro
	130					135					140				
Pro	His	Glu	Ile	Ala	Val	Asn	Ile	Pro	Gly	Phe	Ile	Asp	Ala	Ile	Gln
145					150					155					160
Val	Ile	Pro	Ser	Gly	His	Thr	Ala	Ser	Gly	Gly	Asp	Met	Asn	Thr	Leu
				165					170					175	
Arg	Leu	Gly	Ile	Asp	Gly	Ile	Ser	Gln	Ala	Thr	Pro	Leu	Asp	Thr	Phe
			180					185					190		
Lys	Thr	Ser	Val	Arg	Ala	Gly	His	Ser	Val	Glu	Gln	Ile	Met	Gln	Tyr
		195					200					205			
Pro	Ile	Tyr	Ser	Gly	Ile	Leu	Ala	Gly	Ala	Gly	Trp	Gln	Trp	Val	Asn
	210					215					220				
Leu	Ala	Trp	Leu	Ala	Gly	Gly	Val	Trp	Leu	Leu	Trp	Gln	Lys	Ala	Ile
225					230					235					240
Arg	Trp	His	Ile	Pro	Leu	Ser	Phe	Leu	Val	Thr	Leu	Ala	Leu	Cys	Ala
				245					250					255	
Met	Leu	Gly	Trp	Leu	Phe	Ser	Pro	Glu	Thr	Leu	Ala	Ala	Pro	Gln	Ile
			260					265					270		
His	Leu	Leu	Ser	Gly	Ala	Thr	Met	Leu	Gly	Ala	Phe	Phe	Ile	Leu	Thr
		275					280					285			
Asp	Pro	Val	Thr	Ala	Ser	Thr	Thr	Asn	Arg	Gly	Arg	Leu	Ile	Phe	Gly
	290					295					300				
Ala	Leu	Ala	Gly	Leu	Leu	Val	Trp	Leu	Ile	Arg	Ser	Phe	Gly	Gly	Tyr
305					310					315					320
Pro	Asp	Gly	Val	Ala	Phe	Ala	Val	Leu	Leu	Ala	Asn	Ile	Thr	Val	Pro
				325					330					335	
Leu	Ile	Asp	Tyr	Tyr	Thr	Arg	Pro	Arg	Val	Tyr	Gly	His	Arg	Lys	Gly
			340					345					350		

<210> 194
<211> 206
<212> PRT

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<213> E. Coli

<400> 294
Met Leu Lys Thr Ile Arg Lys His Gly Ile Thr Leu Ala Leu Phe Ala
 1               5                  10                  15
Ala Gly Ser Thr Gly Leu Thr Ala Ala Ile Asn Gln Met Thr Lys Thr
            20                  25                  30
Thr Ile Ala Glu Gln Ala Ser Leu Gln Gln Lys Ala Leu Phe Asp Gln
        35                  40                  45
Val Leu Pro Ala Glu Arg Tyr Asn Asn Ala Leu Ala Gln Ser Cys Tyr
    50                  55                  60
Leu Val Thr Ala Pro Glu Leu Gly Lys Gly Glu His Arg Val Tyr Ile
65                  70                  75                  80
Ala Lys Gln Asp Asp Lys Pro Val Ala Ala Val Leu Glu Ala Thr Ala
                85                  90                  95
Pro Asp Gly Tyr Ser Gly Ala Ile Gln Leu Leu Val Gly Ala Asp Phe
            100                 105                 110
Asn Gly Thr Val Leu Gly Thr Arg Val Thr Glu His His Glu Thr Pro
        115                 120                 125
Gly Leu Gly Asp Lys Ile Glu Leu Arg Leu Ser Asp Trp Ile Thr His
    130                 135                 140
Phe Ala Gly Lys Lys Ile Ser Gly Ala Asp Asp Ala His Trp Ala Val
145                 150                 155                 160
Lys Lys Asp Gly Gly Asp Phe Asp Gln Phe Thr Gly Ala Thr Ile Thr
                165                 170                 175
Pro Arg Ala Val Val Asn Ala Val Lys Arg Ala Gly Leu Tyr Ala Gln
            180                 185                 190
Thr Leu Pro Ala Gln Leu Ser Gln Leu Pro Ala Cys Gly Glu
        195                 200                 205


<210> 295
<211> [illegible]
<212> PRT
<213> E. Coli

<400> 295
Met Ser Glu Ile Lys Asp Val Ile Val Gln Gly Leu Trp Lys Asn Asn
 1               5                  10                  15
Ser Ala Leu Val Gln Leu Leu Gly Leu Cys Pro Leu Leu Ala Val Thr
            20                  25                  30
Ser Thr Ala Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr Thr Leu Val
        35                  40                  45
Leu Thr Leu Thr Asn Leu Thr Ile Ser Thr Leu Arg His Trp Thr Pro
    50                  55                  60
Ala Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala Ser Val Val
65                  70                  75                  80
Ser Ala Val Gln Met Leu Ile Asn Ala Tyr Ala Phe Gly Leu Tyr Gln
                85                  90                  95
Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys Ile Val Val
            100                 105                 110
Gly Arg Ala Glu Ala Phe Ala Ala Lys Lys Gly Pro Ala Leu Ser Ala
        115                 120                 125
Leu Asp Gly Phe Ser Ile Gly Met Gly Ala Thr Cys Ala Met Phe Val
    130                 135                 140
Leu Gly Ser Leu Arg Glu Ile Ile Gly Asn Gly Thr Leu Phe Asp Gly
145                 150                 155                 160
```

Ala Asp Ala Leu Leu Gly Ser Trp Ala Lys Val Leu Arg Val Glu Ile
165 170 175
Phe His Thr Asp Ser Pro Phe Leu Leu Ala Met Leu Pro Pro Gly Ala
180 185 190
Phe Ile Gly Leu Gly Leu Met Leu Ala Gly Lys Tyr Leu Ile Asp Glu
195 200 205
Arg Met Lys Lys Arg Arg Ala Glu Ala Ala Ala Glu Arg Ala Leu Pro
210 215 220
Asn Gly Glu Thr Gly Asn Val
225 230

<210> 196
<211> 111
<212> PRT
<213> E. Coli

<400> 196
Met Asn Lys Ala Lys Arg Leu Glu Ile Leu Thr Arg Leu Arg Glu Asn
1 5 10 15
Asn Pro His Pro Thr Thr Glu Leu Asn Phe Ser Ser Pro Phe Glu Leu
20 25 30
Leu Ile Ala Val Leu Leu Ser Ala Gln Ala Thr Asp Val Ser Val Asn
35 40 45
Lys Ala Thr Ala Lys Leu Tyr Pro Val Ala Asn Thr Pro Ala Ala Met
50 55 60
Leu Glu Leu Gly Val Glu Gly Val Lys Thr Tyr Ile Lys Thr Ile Gly
65 70 75 80
Leu Tyr Asn Ser Lys Ala Glu Asn Ile Ile Lys Thr Cys Arg Ile Leu
85 90 95
Leu Glu Gln His Asn Gly Glu Val Pro Glu Asp Arg Ala Ala Leu Glu
100 105 110
Ala Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val Val Leu Asn Thr
115 120 125
Ala Phe Gly Trp Pro Thr Ile Ala Val Asp Thr His Ile Phe Arg Val
130 135 140
Cys Asn Arg Thr Gln Phe Ala Pro Gly Lys Asn Val Glu Gln Val Glu
145 150 155 160
Glu Lys Leu Leu Lys Val Val Pro Ala Glu Phe Lys Val Asp Cys His
165 170 175
His Trp Leu Ile Leu His Gly Arg Tyr Thr Cys Ile Ala Arg Lys Pro
180 185 190
Arg Cys Gly Ser Cys Ile Ile Glu Asp Leu Cys Glu Tyr Lys Glu Lys
195 200 205
Val Asp Ile
210

<210> 197
<211> 167
<212> PRT
<213> E. Coli

<400> 197
Met Lys Arg Leu His Lys Arg Phe Leu Leu Ala Thr Phe Cys Ala Leu
1 5 10 15
Phe Thr Ala Thr Leu Gln Ala Ala Asp Val Thr Ile Thr Val Asn Gly

```
            20                       25                       30
Arg Val Val Ala Lys Pro Cys Thr Ile Gln Thr Lys Glu Ala Asn Val
        35                      40                      45
Asn Leu Gly Asp Leu Tyr Thr Arg Asn Leu Gln Gln Pro Gly Ser Ala
    50                      55                      60
Ser Gly Trp His Asn Ile Thr Leu Ser Leu Thr Asp Cys Pro Val Glu
65                      70                      75                      80
Thr Ser Ala Val Thr Ala Ile Val Thr Gly Ser Thr Asp Asn Thr Gly
                85                      90                      95
Tyr Tyr Lys Asn Glu Gly Thr Ala Glu Asn Ile Gln Ile Glu Leu Arg
            100                     105                     110
Asp Asp Gln Asp Ala Ala Leu Lys Asn Gly Asp Ser Lys Thr Val Ile
        115                     120                     125
Val Asp Glu Ile Thr Arg Asn Ala Gln Phe Pro Leu Lys Ala Arg Ala
    130                     135                     140
Ile Thr Val Asn Gly Asn Ala Ser Gln Gly Thr Ile Glu Ala Leu Ile
145                     150                     155                     160
Asn Val Ile Tyr Thr Trp Gln
                165


<210> 198
<211> 176
<212> PRT
<213> E. Coli

<400> 198
Met Lys Tyr Asn Asn Ile Ile Phe Leu Gly Leu Cys Leu Gly Leu Thr
 1               5                  10                  15
Thr Tyr Ser Ala Leu Ser Ala Asp Ser Val Ile Lys Ile Ser Gly Arg
            20                  25                  30
Val Leu Asp Tyr Gly Cys Thr Val Ser Ser Asp Ser Leu Asn Phe Thr
        35                  40                  45
Val Asp Leu Gln Lys Asn Ser Ala Arg Gln Phe Pro Thr Thr Gly Ser
    50                  55                  60
Thr Ser Pro Ala Val Pro Phe Gln Ile Thr Leu Ser Glu Cys Ser Lys
65                  70                  75                  80
Gly Thr Thr Gly Val Arg Val Ala Phe Asn Gly Ile Glu Asp Ala Glu
                85                  90                  95
Asn Asn Thr Leu Leu Lys Leu Asp Glu Gly Ser Asn Thr Ala Ser Gly
            100                 105                 110
Leu Gly Ile Gln Ile Leu Asp Ala Asn Met Arg Pro Val Lys Leu Asn
        115                 120                 125
Asp Leu His Ala Gly Met Gln Trp Ile Pro Leu Val Pro Glu Gln Asn
    130                 135                 140
Asn Ile Leu Pro Tyr Ser Ala Arg Leu Lys Ser Thr Gln Lys Ser Val
145                 150                 155                 160
Asn Pro Gly Leu Val Arg Ala Ser Ala Thr Phe Thr Leu Glu Phe Gln
                165                 170                 175


<210> 199
<211> 182
<212> PRT
<213> E. Coli
```

<400> 239

Met Ser Gly Tyr Thr Val Lys Pro Pro Thr Gly Asp Thr Asn Glu Gln
1 5 10 15

Thr Gln Phe Ile Asp Tyr Phe Asn Leu Phe Tyr Ser Lys Arg Gly Gln
20 25 30

Glu Gln Ile Ser Ile Ser Gln Gln Leu Gly Asn Tyr Gly Thr Thr Phe
35 40 45

Phe Ser Ala Ser Arg Gln Ser Tyr Trp Asn Thr Ser Arg Ser Asp Gln
50 55 60

Gln Ile Ser Phe Gly Leu Asn Val Pro Phe Gly Asp Ile Thr Thr Ser
65 70 75 80

Leu Asn Tyr Ser Tyr Ser Asn Asn Ile Trp Gln Asn Asp Arg Asp His
85 90 95

Leu Leu Ala Phe Thr Leu Asn Val Pro Phe Ser His Trp Met Arg Thr
100 105 110

Asp Ser Gln Ser Ala Phe Arg Asn Ser Asn Ala Ser Tyr Ser Met Ser
115 120 125

Asn Asp Leu Lys Gly Gly Met Thr Asn Leu Ser Gly Val Tyr Gly Thr
130 135 140

Leu Leu Pro Asp Asn Asn Leu Asn Tyr Ser Val Gln Val Gly Asn Thr
145 150 155 160

His Gly Gly Asn Thr Ser Ser Gly Thr Ser Gly Tyr Ser Ser Leu Asn
165 170 175

Tyr Arg Gly Ala Tyr Gly Asn Thr Asn Val Gly Tyr Ser Arg Ser Gly
180 185 190

Asp Ser Ser Gln Ile Tyr Tyr Gly Met Ser Gly Gly Ile Ile Ala His
195 200 205

Ala Asp Gly Ile Thr Phe Gly Gln Pro Leu Gly Asp Thr Met Val Leu
210 215 220

Val Lys Ala Pro Gly Ala Asp Asn Val Lys Ile Glu Asn Gln Thr Gly
225 230 235 240

Ile His Thr Asp Trp Arg Gly Tyr Ala Ile Leu Pro Phe Ala Thr Glu
245 250 255

Tyr Arg Glu Asn Arg Val Ala Leu Asn Ala Asn Ser Leu Ala Asp Asn
260 265 270

Val Glu Leu Asp Glu Thr Val Val Thr Val Ile Pro Thr His Gly Ala
275 280 285

Ile Ala Asn Ala Thr Phe Asn Ala Gln Ile Gly Gly Lys Val Leu Met
290 295 300

Thr Leu Lys Tyr Gly Asn Lys Ser Val Pro Phe Gly Ala Ile Val Thr
305 310 315 320

His Gly Gln Asn Lys Asn Gly Ser Ile Val Ala Glu Asn Gly Gln Val
325 330 335

Tyr Leu Thr Gly Leu Pro Gln Ser Gly Gln Leu Gln Val Ser Trp Gly
340 345 350

Lys Asp Lys Asn Ser Asn Cys Ile Val Glu Tyr Lys Leu Pro Glu Val
355 360 365

Ser Pro Gly Thr Leu Leu Asn Gln Gln Thr Ala Ile Cys Arg
370 375 380

<210> 3
<211> 1348
<212> PRT
<213> E. Coli

(400) 300

Met Ile Ala Ile Ala Asp Ile Leu Gln Ala Gly Glu Lys Leu Thr Ala
1 5 10 15
Val Ala Pro Phe Leu Ala Gly Ile Gln Asn Glu Glu Gln Tyr Thr Gln
20 25 30
Ala Leu Gln Leu Val Asp His Leu Leu Leu Asn Asp Pro Glu Asn Pro
35 40 45
Leu Leu Asp Leu Val Cys Ala Lys Ile Thr Ala Trp Glu Glu Ser Ala
50 55 60
Pro Glu Phe Ala Glu Phe Asn Ala Met Ala Gln Ala Met Pro Gly Gly
65 70 75 80
Ile Ala Val Ile Arg Thr Leu Met Asp Gln Tyr Gly Leu Thr Leu Ser
85 90 95
Asp Leu Pro Glu Ile Gly Ser Lys Ser Met Val Ser Arg Val Leu Ser
100 105 110
Gly Lys Arg Lys Leu Thr Leu Glu His Ala Lys Lys Leu Ala Thr Arg
115 120 125
Phe Gly Ile Ser Pro Ala Leu Phe Ile Asp
130 135

(211) 301
(211) 114
(212) PRT
(213) E. Coli

(400) 301

Met His Leu Ile Thr Gln Lys Ala Leu Lys Asp Ala Ala Glu Lys Tyr
1 5 10 15
Pro Gln His Lys Thr Glu Leu Val Ala Leu Gly Asn Thr Ile Ala Lys
20 25 30
Gly Tyr Phe Lys Lys Pro Glu Ser Leu Lys Ala Val Phe Pro Ser Leu
35 40 45
Asp Asn Phe Lys Tyr Leu Asp Lys His Tyr Val Phe Asn Val Gly Gly
50 55 60
Asn Glu Leu Arg Val Val Ala Met Val Phe Phe Glu Ser Gln Lys Cys
65 70 75 80
Tyr Ile Arg Glu Val Met Thr His Lys Glu Tyr Asp Phe Phe Thr Ala
85 90 95
Val His Asn Thr Lys Gly Lys Lys
100

(210) 302
(211) 283
(212) PRT
(213) E. Coli

(400) 302

Met Leu Ser Val Phe Thr Phe Phe Arg Cys Ala Arg Lys Gly Ala Phe
1 5 10 15
Met Leu Ala Arg Ser Gly Lys Val Ser Met Ala Thr Lys Lys Arg Ser
20 25 30
Gly Glu Glu Ile Asn Asp Arg Gln Ile Leu Cys Gly Met Gly Ile Lys
35 40 45
Leu Arg Arg Leu Thr Ala Gly Ile Cys Leu Ile Thr Gln Leu Ala Phe

50 55 60

Pro Met Ala Ala Ala Ala Gln Gly Val Val Asn Ala Ala Thr Gln Gln
65 70 75 80

Pro Val Pro Ala Gln Ile Ala Ile Ala Asn Ala Asn Thr Val Pro Tyr
85 90 95

Thr Leu Gly Ala Leu Glu Ser Ala Gln Ser Val Ala Glu Arg Phe Gly
100 105 110

Ile Ser Val Ala Glu Leu Arg Lys Leu Asn Gln Phe Arg Thr Phe Ala
115 120 125

Arg Ser Phe Asp Asn Val Arg Gln Gly Asp Glu Leu Asp Val Pro Ala
130 135 140

Gln Val Ser Glu Lys Lys Leu Thr Pro Pro Pro Gly Asn Ser Ser Asp
145 150 155 160

Asn Leu Glu Gln Gln Ile Ala Ser Thr Ser Gln Gln Ile Gly Ser Leu
165 170 175

Leu Ala Glu Asp Met Asn Ser Glu Gln Ala Ala Asn Met Ala Arg Gly
180 185 190

Trp Ala Ser Ser Gln Ala Ser Gly Ala Met Thr Asp Trp Leu Ser Arg
195 200 205

Phe Gly Thr Ala Arg Ile Thr Leu Gly Val Asp Glu Arg Pro Ser Leu
210 215 220

Lys Asn Ser Gln Phe Asp Phe Leu His Pro Trp Tyr Glu Thr Pro Asp
225 230 235 240

Asn Leu Phe Phe Ser Gln His Thr Leu His Arg Thr Asp Glu Arg Thr
245 250 255

Gln Ile Asn Asn Gly Leu Gly Trp Arg His Phe Thr Pro Thr Trp Met
260 265 270

Ser Gly Ile Asn Phe Phe Phe Asp His Asp Leu Ser Arg Tyr His Ser
275 280 285

Arg Ala Gly Ile Gly Ala Glu Tyr Trp Arg Asp Tyr Leu Lys Leu Ser
290 295 300

Ser Asn Gly Tyr Leu Arg Leu Thr Asn Trp Arg Ser Ala Pro Glu Leu
305 310 315 320

Asp Asn Asp Tyr Glu Ala Arg Pro Ala Asn Gly Trp Asp Val Arg Ala
325 330 335

Glu Ser Trp Leu Pro Ala Trp Pro His Leu Gly Gly Lys Leu Val Tyr
340 345 350

Glu Gln Tyr Tyr Gly Asp Glu Val Ala Leu Phe Asp Lys Asp Asp Arg
355 360 365

Gln Ser Asn Pro His Ala Ile Thr Ala Gly Leu Asn Tyr Thr Pro Phe
370 375 380

Pro Leu Met Thr Phe Ser Ala Glu Gln Arg Gln Gly Lys Gln Gly Glu
385 390 395 400

Asn Asp Thr Arg Phe Ala Val Asp Phe Thr Trp Gln Pro Gly Ser Ala
405 410 415

Met Gln Lys Gln Leu Asp Pro Asn Glu Val Ala Ala Arg Arg Ser Leu
420 425 430

Ala Gly Ser Arg Tyr Asp Leu Val Asp Arg Asn Asn Asn Ile Val Leu
435 440 445

Glu Tyr Arg Lys Lys Gln Leu Val Arg Leu Thr Leu Thr Asp Pro Val
450 455 460

Thr Gly Lys Ser Gly Glu Val Lys Ser Leu Val Ser Ser Leu Gln Thr
465 470 475 480

Lys Tyr Ala Leu Lys Gly Tyr Asn Val Glu Ala Thr Ala Leu Glu Ala
485 490 495

Ala Gly Gly Lys Val Val Thr Thr Gly Lys Asp Ile Leu Val Thr Leu
500 505 510

Pro Ala Tyr Arg Phe Thr Ser Thr Pro Glu Thr Asp Asn Thr Trp Pro
515 520 525
Ile Glu Val Thr Ala Glu Asp Val Lys Gly Asn Leu Ser Asn Arg Glu
530 535 540
Gln Ser Met Val Val Val Gln Ala Pro Thr Leu Ser Gln Lys Asp Ser
545 550 555 560
Ser Val Ser Leu Ser Thr Gln Thr Leu Asn Ala Asp Ser His Ser Thr
565 570 575
Ala Thr Leu Thr Phe Ile Ala His Asp Ser Ala Ala Gly Asn Pro Val Val
580 585 590
Gly Leu Val Leu Ser Thr Arg His Glu Gly Val Gln Asp Ile Thr Leu
595 600 605
Ser Asp Trp Lys Asp Asn Gly Asp Gly Ser Tyr Thr Gln Ile Leu Thr
610 615 620
Thr Gly Ala Met Ser Gly Thr Leu Thr Leu Met Pro Gln Leu Asn Gly
625 630 635 640
Val Asp Ala Ala Lys Ala Pro Ala Val Val Asn Ile Ile Ser Val Ser
645 650 655
Ser Ser Arg Thr His Ser Ser Ile Lys Ile Asp Lys Asp Asn Tyr Leu
660 665 670
Ser Gly Asn Pro Ile Gln Val Thr Val Glu Leu Arg Asp Glu Asn Asp
675 680 685
Lys Pro Val Lys Glu Gln Lys Gln Gln Leu Asn Asn Ala Val Ser Ile
690 695 700
Asp Asn Val Lys Pro Gly Val Thr Thr Asp Trp Lys Glu Thr Ala Asp
705 710 715 720
Gly Val Tyr Lys Ala Thr Tyr Thr Ala Tyr Thr Lys Gly Ser Gly Leu
725 730 735
Thr Ala Lys Leu Leu Met Gln Asn Trp Asn Glu Asp Leu His Thr Ala
740 745 750
Gly Phe Ile Ile Asp Ala Asn Pro Gln Ser Ala Lys Ile Ala Thr Leu
755 760 765
Ser Ala Ser Asn Asn Gly Val Leu Asn Asn Glu Asn Ala Ala Asn Thr
770 775 780
Val Ser Val Asn Val Ala Asp Glu Gly Ser Asn Pro Ile Asn Asp His
785 790 795 800
Thr Val Thr Phe Ala Val Leu Ser Gly Ser Ala Thr Ser Phe Asn Asn
805 810 815
Gln Asn Thr Ala Lys Thr Asp Val Asn Gly Leu Ala Thr Phe Asp Leu
820 825 830
Lys Ser Ser Lys Gln Glu Asp Asn Thr Val Glu Val Thr Leu Glu Asn
835 840 845
Gly Val Lys Gln Thr Leu Ile Val Ser Phe Val Gly Asp Ser Ser Thr
850 855 860
Ala Gln Val Asp Leu Gln Lys Ser Lys Asn Glu Val Val Ala Asp Gly
865 870 875 880
Asn Asp Ser Val Thr Met Thr Ala Thr Val Arg Asp Ala Lys Gly Asn
885 890 895
Leu Leu Asn Asp Val Met Val Thr Phe Asn Val Asn Ser Ala Glu Ala
900 905 910
Lys Leu Ser Gln Thr Glu Val Asn Ser His Asp Gly Ile Ala Thr Ala
915 920 925
Thr Leu Thr Ser Leu Lys Asn Gly Asp Tyr Arg Val Thr Ala Ser Val
930 935 940
Ser Ser Gly Ser Gln Ala Asn Gln Gln Val Asn Phe Ile Gly Asp Gln
945 950 955 960
Ser Thr Ala Ala Leu Thr Leu Ser Val Pro Ser Gly Asp Ile Thr Val

965 970 975

Thr Asn Thr Ala Pro Gln Tyr Met Thr Ala Thr Leu Gln Asp Lys Asn
980 985 990

Gly Asn Pro Leu Lys Asp Lys Glu Ile Thr Phe Ser Val Pro Asn Asp
995 1000 1005

Val Ala Ser Lys Phe Ser Ile Ser Asn Gly Gly Lys Gly Met Thr Asp
1010 1015 1020

Ser Asn Gly Val Ala Ile Ala Ser Leu Thr Gly Thr Leu Ala Gly Thr
1025 1030 1035 1040

His Met Ile Met Ala Arg Leu Ala Asn Ser Asn Val Ser Asp Ala Gln
1045 1050 1055

Pro Met Thr Phe Val Ala Asp Lys Asp Arg Ala Val Val Val Leu Gln
1060 1065 1070

Thr Ser Lys Ala Glu Ile Ile Gly Asn Gly Val Asp Glu Thr Thr Leu
1075 1080 1085

Thr Ala Thr Val Lys Asp Pro Ser Asn His Pro Val Ala Gly Ile Thr
1090 1095 1100

Val Asn Phe Thr Met Pro Gln Asp Val Ala Ala Asn Phe Thr Leu Glu
1105 1110 1115 1120

Asn Asn Gly Ile Ala Ile Thr Gln Ala Asn Gly Glu Ala His Val Thr
1125 1130 1135

Leu Lys Gly Lys Lys Ala Gly Thr His Thr Val Thr Ala Thr Leu Gly
1140 1145 1150

Asn Asn Asn Thr Ser Asp Ser Gln Pro Val Thr Phe Val Ala Asp Lys
1155 1160 1165

Ala Ser Ala Gln Val Val Leu Gln Ile Ser Lys Asp Glu Ile Thr Gly
1170 1175 1180

Asn Gly Val Asp Ser Ala Thr Leu Thr Ala Thr Val Lys Asp Gln Phe
1185 1190 1195 1200

Asp Asn Glu Val Asn Asn Leu Pro Val Thr Phe Ser Ser Ala Ser Ser
1205 1210 1215

Gly Leu Thr Leu Thr Pro Gly Val Ser Asn Thr Asn Gln Ser Gly Ile
1220 1225 1230

Ala Gln Ala Thr Leu Ala Gly Val Ala Phe Gly Glu Lys Thr Val Thr
1235 1240 1245

Ala Ser Leu Ala Asn Asn Gly Ala Ser Asp Asn Lys Thr Val His Phe
1250 1255 1260

Ile Gly Asp Thr Ala Ala Ala Lys Ile Ile Glu Leu Ala Pro Val Pro
1265 1270 1275 1280

Asp Ser Ile Ile Ala Gly Thr Pro Gln Asn Ser Ser Gly Ser Val Ile
1285 1290 1295

Thr Ala Thr Val Val Asp Asn Asn Gly Phe Pro Val Lys Gly Val Thr
1300 1305 1310

Val Asn Phe Thr Ser Asn Ala Ala Thr Ala Glu Met Thr Asn Gly Gly
1315 1320 1325

Gln Ala Val Thr Asn Glu Gln Gly Lys Ala Thr Val Thr Tyr Thr Asn
1330 1335 1340

Thr Arg Ser Ser Ile Glu Ser Gly Ala Arg Pro Asp Thr Val Glu Ala
1345 1350 1355 1360

Ser Leu Glu Asn Gly Ser Ser Thr Leu Ser Thr Ser Ile Asn Val Asn
1365 1370 1375

Ala Asp Ala Ser Thr Ala His Leu Thr Leu Leu Gln Ala Leu Phe Asp
1380 1385 1390

Thr Val Ser Ala Gly Glu Thr Thr Ser Leu Tyr Ile Glu Val Lys Asp
1395 1400 1405

Asn Tyr Gly Asn Gly Val Pro Gln Gln Glu Val Thr Leu Ser Val Ser
1410 1415 1420

Pro Ser Glu Gly Val Thr Pro Ser Asn Asn Ala Ile Tyr Thr Thr Asn
1425 1430 1435 1440
His Asp Gly Asn Phe Tyr Ala Ser Phe Thr Ala Thr Lys Ala Gly Val
1445 1450 1455
Tyr Gln Leu Thr Ala Thr Leu Glu Asn Gly Asp Ser Met Gln Gln Thr
1460 1465 1470
Val Thr Tyr Val Pro Asn Val Ala Asn Ala Glu Ile Thr Leu Ala Ala
1475 1480 1485
Ser Lys Asp Pro Val Ile Ala Asp Asn Asn Asp Leu Thr Thr Leu Thr
1490 1495 1500
Ala Thr Val Ala Asp Thr Glu Gly Asn Ala Ile Ala Asn Thr Glu Val
1505 1510 1515 1520
Thr Phe Thr Leu Pro Glu Asp Val Lys Ala Asn Phe Thr Leu Ser Asp
1525 1530 1535
Gly Gly Lys Val Ile Thr Asp Ala Glu Gly Lys Ala Lys Val Thr Leu
1540 1545 1550
Lys Gly Thr Lys Ala Gly Ala His Thr Val Thr Ala Ser Met Thr Gly
1555 1560 1565
Gly Lys Ser Glu Gln Leu Val Val Asn Phe Ile Ala Asp Thr Leu Thr
1570 1575 1580
Ala Gln Val Asn Leu Asn Val Thr Gln Asp Asn Phe Ile Ala Asn Asn
1585 1590 1595 1600
Val Gly Met Thr Arg Leu Gln Ala Thr Val Thr Asp Gly Asn Gly Asn
1605 1610 1615
Pro Leu Ala Asn Glu Ala Val Thr Phe Thr Leu Pro Ala Asp Val Ser
1620 1625 1630
Ala Ser Phe Thr Leu Gly Gln Gly Gly Ser Ala Ile Thr Asp Ile Asn
1635 1640 1645
Gly Lys Ala Glu Val Thr Leu Ser Gly Thr Lys Ser Gly Thr Tyr Pro
1650 1655 1660
Val Thr Val Ser Val Asn Asn Tyr Gly Val Ser Asp Thr Lys Gln Val
1665 1670 1675 1680
Thr Leu Ile Ala Asp Ala Gly Thr Ala Lys Leu Ala Ser Leu Thr Ser
1685 1690 1695
Val Tyr Ser Phe Val Val Ser Thr Thr Glu Gly Ala Thr Met Thr Ala
1700 1705 1710
Ser Val Thr Asp Ala Asn Gly Asn Pro Val Glu Gly Ile Lys Val Asn
1715 1720 1725
Phe Arg Gly Thr Ser Val Thr Leu Ser Ser Thr Ser Val Glu Thr Asp
1730 1735 1740
Asp Arg Gly Phe Ala Glu Ile Leu Val Thr Ser Thr Glu Val Gly Leu
1745 1750 1755 1760
Lys Thr Val Ser Ala Ser Leu Ala Asp Lys Pro Thr Glu Val Ile Ser
1765 1770 1775
Arg Leu Leu Asn Ala Ser Ala Asp Val Asn Ser Ala Thr Ile Thr Ser
1780 1785 1790
Leu Glu Ile Pro Glu Gly Gln Val Met Val Ala Gln Asp Val Ala Val
1795 1800 1805
Lys Ala His Val Asn Asp Gln Phe Gly Asn Pro Val Ala His Gln Pro
1810 1815 1820
Val Thr Phe Ser Ala Glu Pro Ser Ser Gln Met Ile Ile Ser Gln Asn
1825 1830 1835 1840
Thr Val Ser Thr Asn Thr Gln Gly Val Ala Glu Val Thr Met Thr Pro
1845 1850 1855
Glu Arg Asn Gly Ser Tyr Met Val Lys Ala Ser Leu Pro Asn Gly Ala
1860 1865 1870
Ser Leu Glu Lys Gln Leu Glu Ala Ile Asp Glu Lys Leu Thr Leu Thr

```
        1975                1980                1985
Ala Ser Ser Pro Leu Ile Gly Val Tyr Ala Pro Thr Gly Ala Thr Leu
    1990                1995                2000
Thr Ala Thr Leu Thr Ser Ala Asn Gly Thr Pro Val Glu Gly Gln Val
2005                2010                2015                2020
Ile Asn Phe Ser Val Thr Pro Glu Gly Ala Thr Leu Ser Gly Gly Lys
                2025                2030                2035
Val Arg Thr Asn Ser Ser Gly Gln Ala Pro Val Val Leu Thr Ser Asn
            2040                2045                2050
Lys Val Gly Thr Tyr Thr Val Thr Ala Ser Phe His Asn Gly Val Thr
        2055                2060                2065
Ile Gln Thr Gln Thr Thr Val Lys Val Thr Gly Asn Ser Ser Thr Ala
    2070                2075                2080
His Val Ala Ser Phe Ile Ala Asp Pro Ser Thr Ile Ala Ala Thr Asn
2085                2090                2095                2100
Thr Asp Leu Ser Thr Leu Lys Ala Thr Val Glu Asp Gly Ser Gly Asn
                2105                2110                2115
Leu Ile Glu Gly Leu Thr Val Tyr Phe Ala Leu Lys Ser Gly Ser Ala
            2120                2125                2130
Thr Leu Thr Ser Leu Thr Ala Val Thr Asp Gln Asn Gly Ile Ala Thr
        2135                2140                2145
Thr Ser Val Lys Gly Ala Met Thr Gly Ser Val Thr Val Ser Ala Val
    2150                2155                2160
Thr Thr Ala Gly Gly Met Gln Thr Val Asp Ile Thr Leu Val Ala Gly
2165                2170                2175                2180
Pro Ala Asp Thr Ser Gln Ser Val Leu Lys Ser Asn Arg Ser Ser Leu
                2185                2190                2195
Lys Gly Asp Tyr Thr Asp Ser Ala Glu Leu Arg Val Leu His Asp
            2200                2205                2210
Ile Ser Gly Asn Pro Ile Lys Val Ser Glu Gly Met Gln Phe Val Gln
        2215                2220                2225
Ser Gly Thr Asn Val Pro Tyr Ile Lys Ile Ser Ala Ile Asp Tyr Ser
    2230                2235                2240
Leu Asn Ile Asn Gly Asp Tyr Lys Ala Thr Val Thr Gly Gly Gly Gln
2245                2250                2255                2260
Gly Ile Ala Thr Leu Ile Pro Val Leu Asn Gly Val His Gln Ala Gly
                2265                2270                2275
Leu Ser Thr Thr Ile Gln Phe Thr Asn Ala Glu Asp Lys Ile Met Ser
            2280                2285                2290
Gly Thr Val Ser Val Asn Gly Thr Asp Leu Pro Thr Thr Thr Phe Pro
        2295                2300                2305
Ser Gln Gly Pro Thr Gly Ala Tyr Tyr Gln Leu Asn Asn Asp Asn Phe
    2310                2315                2320
Ala Pro Gly Lys Thr Ala Ala Asp Tyr Glu Phe Ser Ser Ser Ala Ser
2325                2330                2335                2340
Trp Val Asp Val Asp Ala Thr Gly Lys Val Thr Phe Lys Asn Val Gly
                2345                2350                2355
Ser Asn Ser Glu Asp Ile Thr Ala Thr Pro Lys Ser Gly Gly Pro Ser
            2360                2365                2370
Tyr Val Tyr Glu Ile Arg Val Lys Ser Trp Trp Val Asn Ala Gly Gln
        2375                2380                2385
Ala Phe Met Ile Tyr Ser Leu Ala Glu Asn Phe Cys Ser Ser Asn Gly
    2390                2395                2400
Tyr Thr Leu Pro Arg Ala Asn Tyr Leu Asn His Cys Ser Ser Arg Gly
2405                2410                2415                2420
Ile Gly Ser Leu Tyr Ser Glu Trp Gly Asp Met Gly His Tyr Thr Thr
                2425                2430                2435
```

Asp Ala Gly Phe Gln Ser Asn Met Tyr Trp Ser Ser Ser Pro Ala Asn
2340 2345 2350
Ser Ser Glu Gln Tyr Val Val Ser Leu Ala Thr Gly Asp Gln Ser Val
2355 2360 2365
Phe Glu Lys Leu Gly Phe Ala Tyr Ala Thr Cys Tyr Lys Asn Leu
2370 2375 2380

<200> 403
<211> 61
<212> PRT
<213> E. Coli

<400> 403
Met Ser Lys Gly Ala Leu Tyr Glu Phe Asn Asn Pro Asp Gln Leu Lys
1 5 10 15
Ile Pro Leu Pro His Lys His Ile Ala Ser Thr Phe Asn Asp Ile Met
20 25 30
Ser Lys Asp Val Gly Tyr Ala Tyr Val Ser Leu Leu Tyr Ala Cys Pro
35 40 45
Leu Lys Thr His Ser Leu Arg Leu Asn Pro Phe Ser Lys
50 55 60

<210> 404
<211> 499
<212> PRT
<213> E. Coli

<400> 404
Met Gln Val Ala Glu Gln Arg Ile Gln Leu Ala Glu Ala Gln Ala Lys
1 5 10 15
Ala Val Ala Thr Gln Asp Gly Pro Gln Ile Asp Phe Ser Ala Asp Met
20 25 30
Glu Arg Gln Lys Met Ser Ala Glu Gly Leu Met Gly Pro Phe Ala Leu
35 40 45
Asn Asp Pro Ala Ala Gly Thr Thr Gly Pro Trp Tyr Thr Asn Gly Thr
50 55 60
Phe Gly Leu Thr Ala Gly Trp His Leu Asp Ile Trp Gly Lys Asn Arg
65 70 75 80
Ala Gln Val Thr Ala Arg Leu Gly Thr Val Lys Ala Arg Ala Ala Glu
85 90 95
Arg Gln Gln Thr Arg Gln Leu Leu Ala Gly Ser Val Ala Arg Leu Tyr
100 105 110
Trp Gln Trp Gln Thr Gln Ala Ala Leu Asn Thr Val Leu Gln Gln Ile
115 120 125
Glu Lys Glu Gln Asn Thr Ile Ile Ala Thr Asp Arg Gln Leu Tyr Gln
130 135 140
Asn Gly Ile Thr Ser Ser Val Glu Gly Val Glu Thr Asp Ile Asn Ala
145 150 155 160
Ser Lys Thr Arg Gln Gln Leu Asn Asp Val Ala Gly Lys Met Lys Ile
165 170 175
Ile Glu Ala Arg Leu Ser Ala Leu Thr Asn Asn Gln Thr Lys Ser Leu
180 185 190
Lys Leu Lys Pro Val Ala Leu Pro Lys Val Ala Ser Gln Leu Pro Asp
195 200 205
Glu Leu Gly Tyr Ser Leu Leu Ala Arg Arg Ala Asp Leu Gln Ala Ala

```
     210                 215                 220
His Trp Tyr Val Glu Ser Ser Leu Ser Thr Ile Asp Ala Ala Lys Ala
225                 230                 235                 240
Ala Phe Tyr Pro Asp Ile Asn Leu Met Ala Phe Leu Gln Gln Asp Ala
                245                 250                 255
Leu His Leu Ser Asp Leu Phe Arg His Ser Ala Gln Gln Met Gly Val
            260                 265                 270
Thr Ala Gly Leu Thr Leu Pro Ile Phe Asp Ser Gly Arg Leu Asn Ala
        275                 280                 285
Asn Leu Asp Ile Ala Lys Ala Glu Ser Asn Leu Ser Ile Ala Ser Tyr
    290                 295                 300
Asn Lys Ala Val Val Glu Ala Val Asn Asp Val Ala Arg Ala Ala Ser
305                 310                 315                 320
Gln Val Gln Thr Leu Ala Glu Lys Asn Gln His Gln Ala Gln Ile Glu
                325                 330                 335
Arg Asp Ala Leu Arg Val Val Gly Leu Ala Gln Ala Arg Phe Asn Ala
            340                 345                 350
Gly Ile Ile Ala Gly Ser Arg Val Ser Glu Ala Arg Ile Pro Ala Leu
        355                 360                 365
Arg Glu Arg Ala Asn Gly Leu Leu Leu Gln Gly Gln Trp Leu Asp Ala
    370                 375                 380
Ser Ile Gln Leu Thr Gly Ala Leu Gly Gly Gly Tyr Lys Arg
385                 390                 395
```


(21) 395
(21) 96
(21) PRT
(21) E. Coli


```
(2) 395
Met Tyr Lys His Ala Lys Leu Lys Asn Ile Ser Gln His Thr Val Ile
 1               5                  10                  15
Ser Ala His Leu Phe Leu Pro Asp Tyr Ser Pro Met Asn Arg Asp Ser
            20                  25                  30
Phe Tyr Pro Ala Ile Ala Cys Phe Pro Leu Leu Leu Met Leu Ala Gly
        35                  40                  45
Cys Ala Pro Met His Glu Thr Arg Gln Ala Leu Ser Gln Gln Thr Pro
    50                  55                  60
Ala Ala Gln Val Asp Thr Ala Leu Pro Thr Ala Leu Lys Met Val Gly
65                  70                  75                  80
Gln Thr Ala Asn Gly Gly Trp Ser Ile Thr Ile Ile Asn Ser Leu Pro
                85                  90                  95
```


(21) 396
(21) 132
(21) PRT
(21) E. Coli


```
(40) 396
Met Arg Val Leu Leu Ala Pro Met Glu Gly Val Leu Asp Ser Leu Val
 1               5                  10                  15
Arg Glu Leu Leu Thr Glu Val Asn Asp Tyr Asp Leu Cys Ile Thr Glu
            20                  25                  30
Phe Val Arg Val Val Asp Gln Leu Leu Pro Val Lys Val Phe His Arg
        35                  40                  45
```

Ile Cys Pro Glu Leu Gln Asn Ala Ser Arg Thr Pro Ser Gly Thr Leu
50 55 60
Val Arg Val Gln Leu Leu Gly Gln Pro Pro Gln Trp Leu Ala Glu Asn
65 70 75 80
Ala Ala Arg Ala Val Glu Leu Gly Ser Trp Gly Val Asp Leu Asn Cys
85 90 95
Gly Cys Pro Ser Lys Thr Val Asn Gly Ser Gly Gly Gly Ala Thr Leu
100 105 110
Leu Lys Asp Pro Glu Leu Ile Tyr Gln Gly Ala Lys Ala Met Arg Glu
115 120 125
Ala Val Pro Ala His Leu Pro Val Ser Val Lys Val Arg Leu Gly Trp
130 135 140
Asp Ser Gly Glu Lys Lys Phe Glu Ile Ala Asp Ala Val Gln Gln Ala
145 150 155 160
Gly Ala Thr Glu Leu Val Val His Gly Arg Thr Lys Glu Gln Gly Tyr
165 170 175
Arg Ala Glu His Ile Asp Trp Gln Ala Ile Gly Asp Ile Arg Gln Arg
180 185 190
Leu Asn Ile Pro Val Ile Ala Asn Gly Glu Ile Trp Asp Trp Gln Ser
195 200 205
Ala Gln Gln Cys Met Ala Ile Ser Gly Cys Asp Ala Val Met Ile Gly
210 215 220
Arg Gly Ala Leu Asn Ile Pro Asn Leu Ser Arg Val Val Lys Tyr Asn
225 230 235 240
Glu Pro Arg Met Pro Trp Pro Glu Val Val Ala Leu Leu Gln Lys Tyr
245 250 255
Thr Asn Leu Glu Lys Gln Gly Asp Thr Gly Leu Tyr His Val Ala Arg
260 265 270
Ile Lys Gln Trp Leu Ser Tyr Leu Arg Lys Glu Tyr Asp Glu Ala Thr
275 280 285
Glu Leu Phe Gln His Val Arg Val Leu Asn Asn Ser Pro Asp Ile Ala
290 295 300
Arg Ala Ile Gln Ala Ile Asp Ile Glu Lys Leu
305 310 315

<210> 607
<211> 796
<212> PRT
<213> E. Coli

<400> 607
Met Thr Ile Ser Thr Thr Ser Thr Pro His Asp Ala Val Phe Lys Ser
1 5 10 15
Phe Leu Arg His Pro Asp Thr Ala Arg Asp Phe Ile Asp Ile His Leu
20 25 30
Pro Ala Pro Leu Arg Lys Leu Cys Asp Leu Thr Thr Leu Lys Leu Glu
35 40 45
Pro Asn Ser Phe Ile Asp Glu Asp Leu Arg Gln Tyr Tyr Ser Asp Leu
50 55 60
Leu Trp Ser Val Lys Thr Gln Glu Gly Val Gly Tyr Ile Tyr Val Val
65 70 75 80
Ile Glu His Gln Ser Lys Pro Glu Gln Leu Met Ala Phe Arg Met Met
85 90 95
Arg Tyr Ser Ile Ala Ala Met Gln Asn His Leu Asp Ala Gly Tyr Lys
100 105 110
Glu Leu Pro Leu Val Leu Pro Met Leu Phe Tyr His Gly Cys Arg Ser

```
        115                 120                 125
Pro Tyr Pro Tyr Ser Leu Cys Trp Leu Asp Glu Phe Ala Glu Pro Ala
    130                 135                 140
Ile Ala Arg Lys Ile Tyr Ser Ser Ala Phe Pro Leu Val Asp Ile Thr
145                 150                 155                 160
Val Val Pro Asp Asp Glu Ile Met Gln His Arg Lys Met Ala Leu Leu
                165                 170                 175
Glu Leu Ile Gln Lys His Ile Arg Gln Arg Asp Leu Leu Gly Leu Val
            180                 185                 190
Asp Gln Ile Val Ser Leu Leu Val Thr Gly Asn Thr Asn Asp Arg Gln
        195                 200                 205
Leu Lys Ala Leu Phe Asn Tyr Val Leu Gln Thr Gly Asp Ala Gln Arg
    210                 215                 220
Phe Arg Ala Phe Ile Gly Glu Ile Ala Glu Arg Ala Pro Gln Glu Lys
225                 230                 235                 240
Glu Lys Leu Met Thr Ile Ala Asp Arg Leu Arg Glu Glu Gly Ala Met
                245                 250                 255
Gln Gly Lys His Glu Glu Ala Leu Arg Ile Ala Gln Glu Met Leu Asp
            260                 265                 270
Arg Gly Leu Asp Arg Glu Leu Val Met Met Val Thr Arg Leu Ser Pro
        275                 280                 285
Asp Asp Leu Ile Ala Gln Ser His
    290                 295
```

<210> 308
<211> 888
<212> PRT
<213> E. Coli

<400> 308

```
<400> 8
Met Ala Gln Phe Val Tyr Thr Met His Arg Val Gly Lys Val Val Pro
 1               5                  10                  15
Pro Lys Arg His Ile Leu Lys Asn Ile Ser Leu Ser Phe Phe Pro Gly
            20                  25                  30
Ala Lys Ile Gly Val Leu Gly Leu Asn Gly Ala Gly Lys Ser Thr Leu
        35                  40                  45
Leu Arg Ile Met Ala Gly Ile Asp Lys Asp Ile Glu Gly Glu Ala Arg
    50                  55                  60
Pro Gln Pro Asp Ile Lys Ile Gly Tyr Leu Pro Gln Glu Pro Gln Leu
65                  70                  75                  80
Asn Pro Glu His Thr Val Arg Glu Ser Ile Glu Gln Ala Val Ser Glu
                85                  90                  95
Val Val Asn Ala Leu Lys Arg Leu Asp Glu Val Tyr Ala Leu Tyr Ala
            100                 105                 110
Asp Pro Asp Ala Asp Phe Asp Lys Leu Ala Ala Glu Gln Gly Arg Leu
        115                 120                 125
Glu Glu Ile Ile Gln Ala His Asp Gly His Asn Leu Asn Val Gln Leu
    130                 135                 140
Glu Arg Ala Ala Asp Ala Leu Arg Leu Pro Asp Trp Asp Ala Lys Ile
145                 150                 155                 160
Ala Asn Leu Ser Gly Gly Glu Arg Arg Arg Val Ala Leu Cys Arg Leu
                165                 170                 175
Leu Leu Glu Lys Pro Asp Met Leu Leu Leu Asp Glu Pro Thr Asn His
            180                 185                 190
Leu Asp Ala Glu Ser Val Ala Trp Leu Glu Arg Phe Leu His Asp Phe
```

```
        195                 200                 205
Glu Gly Thr Val Val Ala Ile Thr His Asp Arg Tyr Phe Leu Asp Asn
    210                 215                 220
Val Ala Gly Trp Ile Leu Glu Leu Asp Arg Gly Glu Gly Ile Pro Trp
225                 230                 235                 240
Glu Gly Asn Tyr Ser Ser Trp Leu Glu Gln Lys Asp Gln Arg Leu Ala
                245                 250                 255
Gln Glu Ala Ser Gln Gln Ala Ala Arg Arg Lys Ser Ile Glu Lys Glu
            260                 265                 270
Leu Gln Trp Val Arg Gln Gly Thr Lys Gly Arg Gln Ser Lys Gly Lys
        275                 280                 285
Ala Arg Leu Ala Arg Phe Glu Glu Leu Asn Ser Thr Glu Tyr Gln Lys
    290                 295                 300
Arg Asn Gln Thr Asn Glu Leu Phe Ile Pro Pro Gly Pro Arg Leu Gly
305                 310                 315                 320
Asp Lys Val Leu Glu Val Ser Asn Leu Arg Lys Ser Tyr Gly Asp Arg
                325                 330                 335
Leu Leu Ile Asp Asp Leu Ser Phe Ser Ile Pro Lys Gly Ala Ile Val
            340                 345                 350
Gly Ile Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Phe Arg Met
        355                 360                 365
Ile Ser Gly Gln Glu Gln Pro Asp Ser Gly Thr Ile Thr Leu Gly Glu
    370                 375                 380
Thr Val Lys Leu Ala Ser Val Asp Gln Phe Arg Asp Ser Met Asp Asn
385                 390                 395                 400
Ser Lys Thr Val Trp Glu Glu Val Ser Gly Gly Leu Asp Ile Met Lys
                405                 410                 415
Ile Gly Asn Thr Glu Met Pro Ser Arg Ala Tyr Val Gly Arg Phe Asn
            420                 425                 430
Phe Lys Gly Val Asp Gln Gly Lys Arg Val Gly Glu Leu Ser Gly Gly
        435                 440                 445
Glu Arg Gly Arg Leu His Leu Ala Lys Leu Leu Gln Val Gly Gly Asn
    450                 455                 460
Met Leu Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Glu Thr Leu
465                 470                 475                 480
Arg Ala Leu Glu Asn Ala Leu Leu Glu Phe Pro Gly Cys Ala Met Val
                485                 490                 495
Ile Ser His Asp Arg Trp Phe Leu Asp Arg Ile Ala Thr His Ile Leu
            500                 505                 510
Asp Tyr Gln Asp Gln Gly Lys Val Glu Phe Phe Glu Gly Asn Phe Thr
        515                 520                 525
Glu Tyr Glu Glu Tyr Lys Lys Arg Thr Leu Gly Ala Asp Ala Leu Glu
    530                 535                 540
Pro Lys Arg Ile Lys Tyr Lys Arg Ile Ala Lys
545                 550
```

<210> 309
<211> 173
<212> PRT
<213> E. Coli

<400> 309

```
Met Ser Lys Pro Lys Tyr Pro Phe Glu Lys Arg Leu Glu Val Val Asn
 1               5                  10                  15
His Tyr Phe Thr Thr Asp Asp Gly Tyr Arg Ile Ile Ser Ala Arg Phe
```

```
                20                  25                  30
Gly Val Pro Arg Thr Gln Val Arg Thr Trp Val Ala Leu Tyr Glu Lys
            35                  40                  45
His Gly Glu Lys Gly Leu Ile Pro Lys Pro Lys Gly Val Ser Ala Asp
        50                  55                  60
Pro Glu Leu Arg Ile Lys Val Val Lys Ala Val Ile Glu Gln His Met
65                  70                  75                  80
Ser Leu Asn Gln Ala Ala Ala His Phe Met Leu Ala Gly Ser Gly Ser
                85                  90                  95
Val Ala Arg Trp Leu Lys Val Tyr Glu Glu Arg Gly Glu Ala Gly Leu
            100                 105                 110
Arg Ala Leu Lys Ile Gly Thr Lys Arg Asn Ile Ala Ile Ser Val Asp
        115                 120                 125
Pro Glu Lys Ala Ala Ser Ala Leu Glu Leu Ser Lys Asp Arg Arg Ile
    130                 135                 140
Glu Asp Leu Glu Arg Gln Val Arg Phe Leu Glu Thr Arg Leu Met Tyr
145                 150                 155                 160
Leu Lys Lys Leu Lys Ala Leu Ala His Pro Thr Lys Lys
                165                 170
```

<220> 210

<211> 243

<212> DNA

<213> E. Coli

<400> 210

```
Met Lys Val Leu Asn Glu Leu Arg Gln Phe Tyr Pro Leu Asp Glu Leu
 1               5                  10                  15
Leu Arg Ala Ala Glu Ile Pro Arg Ser Thr Phe Tyr Tyr His Leu Lys
            20                  25                  30
Ala Leu Ser Lys Pro Asp Lys Tyr Ala Asp Val Lys Lys Arg Ile Ser
        35                  40                  45
Glu Ile Tyr His Glu Asn Arg Gly Arg Tyr Gly Tyr Arg Arg Val Thr
    50                  55                  60
Leu Ser Leu His Arg Glu Gly Lys Gln Ile Asn His Lys Ala Val Gln
65                  70                  75                  80
Arg Leu Met Gly Thr Leu Ser Leu Lys Ala Ala Ile Lys Val Lys Arg
                85                  90                  95
Tyr Arg Ser Tyr Arg Gly Glu Val Gly Gln Thr Ala Pro Asn Val Leu
            100                 105                 110
Gln Arg Asp Phe Lys Ala Thr Arg Pro Asn Glu Lys Trp Val Thr Asp
        115                 120                 125
Val Thr Glu Phe Ala Val Asn Gly Arg Lys Leu Tyr Leu Ser Pro Val
    130                 135                 140
Ile Asp Leu Phe Asn Asn Glu Val Ile Ser Tyr Ser Leu Ser Glu Arg
145                 150                 155                 160
Pro Val Met Asn Met Val Glu Asn Met Leu Asp Gln Ala Phe Lys Lys
                165                 170                 175
Leu Asn Pro His Glu His Pro Val Leu His Ser Asp Gln Gly Trp Gln
            180                 185                 190
Tyr Arg Met Arg Arg Tyr Gln Asn Ile Leu Lys Glu His Gly Ile Lys
        195                 200                 205
Gln Ser Met Ser Arg Lys Gly Asn Cys Leu Asp Asn Ala Val Val Glu
    210                 215                 220
Cys Phe Phe Gly Thr Leu Lys Ser Glu Cys Phe Tyr Leu Asp Glu Phe
225                 230                 235                 240
```

Ser Asn Ile Ser Glu Leu Lys Asp Ala Val Thr Glu Tyr Ile Glu Tyr
245 250 255
Tyr Asn Ser Arg Arg Ile Ser Leu Lys Leu Lys Gly Leu Thr Pro Ile
260 265 270
Glu Tyr Arg Asn Gln Thr Tyr Met Pro Arg Val
275 280

<211> 311
<212> DNA
<213> E. Coli

<400> 311

Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
1 5 10 15
Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
20 25 30
His Lys Gln Arg Gln Gly
35

<211> 312
<212> DNA
<213> E. Coli

<400> 312

Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
1 5 10 15
Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
20 25 30
Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
35 40 45
Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe
50 55 60
Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu
65 70 75 80
Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr
85 90 95
Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly
100 105 110
Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala
115 120 125
Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly
130 135 140
Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala
145 150 155 160
Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu
165 170 175
Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe
180 185 190
Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu
195 200 205
Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Leu Val Ala
210 215 220
Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly
225 230 235 240

Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg
245 250 255
Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala
260 265 270
Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala
275 280 285
Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
290 295 300
Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
305 310 315 320
Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
325 330 335
Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe
340 345 350
Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys
355 360 365
Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile
370 375 380
Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr
385 390 395 400
Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe
405 410 415
Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
420 425 430
Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg
435 440

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144
(B) TYPE: PRT
(C) STRANDEDNESS:
(D) TOPOLOGY: E. Coli

(ii) MOLECULE TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly
1 5 10 15
Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly
20 25 30
Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Gly Val Arg Arg
35 40 45
Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe
50 55 60
Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser
65 70 75 80
Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys
85 90 95
Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu
100 105 110
Ala Gly Glu Val Thr Thr Pro Val Thr Val Arg Gly Leu Arg Val Thr
115 120 125
Lys Gly Ala Arg Ala Ala Ile Glu Ala Ala Gly Gly Lys Ile Glu Glu
130 135 140

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90

(213) PRT
(213) E. Coli

(400) 314
Met Ala Lys Thr Ile Lys Ile Thr Gln Thr Arg Ser Ala Ile Gly Arg
1 5 10 15
Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile
20 25 30
Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile
35 40 45
Asn Ala Val Ser Phe Met Val Lys Val Glu Glu
50 55

(210) 315
(211) 167
(212) PRT
(213) E. Coli

(400) 315
Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile
1 5 10 15
Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser
20 25 30
Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe
35 40 45
Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met
50 55 60
Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr
65 70 75 80
Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met
85 90 95
Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg
100 105 110
Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
115 120 125
Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
130 135 140
Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
145 150 155 160
Val Glu Glu Ile Leu Gly Lys
165

(210) 316
(211) 117
(212) PRT
(213) E. Coli

(400) 316
Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
1 5 10 15
Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
20 25 30
Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu
35 40 45

Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr
50 55 60
Thr Gly Asn Lys Asp Ala Ala Ala Ala Val Gly Lys Ala Val Ala Glu
65 70 75 80
Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly
85 90 95
Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu
100 105 110
Ala Gly Leu Gln Phe
115

<210> 317
<211> 177
<212> PRT
<213> E. Coli

<400> 317
Met Ser Asn Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
1 5 10 15
Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
20 25 30
Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
35 40 45
Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
50 55 60
Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
65 70 75 80
Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
85 90 95
Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
100 105 110
Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
115 120 125
Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val
130 135 140
Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
145 150 155 160
Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
165 170 175
Lys

<210> 318
<211> 180
<212> PRT
<213> E. Coli

<400> 318
Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn
1 5 10 15
Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu
20 25 30
Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp
35 40 45
Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys

```
     50                  55                  60
Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg
65                  70                  75                  80
Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met
                85                  90                  95
Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr
            100                 105                 110
Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr
        115                 120                 125
Val Ala
    130
```


(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRAND: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: PRT

(vi) ORIGINAL SOURCE: E. Coli

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:


```
Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
 1               5                  10                  15
Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
            20                  25                  30
Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
        35                  40                  45
Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
    50                  55                  60
Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
65                  70                  75                  80
Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
                85                  90                  95
Lys Lys Ala Ser Trp
            100
```


(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117

(B) TYPE: amino acid

(C) STRAND: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: PRT

(vi) ORIGINAL SOURCE: E. Coli

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:


```
Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu
 1               5                  10                  15
Met Thr Gln Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu
            20                  25                  30
Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys
        35                  40                  45
Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys
    50                  55                  60
Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg
65                  70                  75                  80
Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met
                85                  90                  95
Trp Gln Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg
            100                 105                 110
Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr
```

```
        115                 120                 125
Ser Met Gly Val Arg Glu Gln Ile Ile Phe Pro Glu Ile Asp Tyr Asp
    130                 135                 140
Lys Val Asp Arg Val Arg Gly Leu Asp Ile Thr Ile Thr Thr Thr Ala
145                 150                 155                 160
Lys Ser Asp Glu Glu Gly Arg Ala Leu Leu Ala Ala Phe Asp Phe Pro
                165                 170                 175
Phe Arg Lys
```

<210> 312
<211> 104
<212> PRT
<213> E. Coli

<400> [illegible]

```
Met Ala Ala Lys Ile Arg Arg Asp Asp Glu Val Ile Val Leu Thr Gly
 1               5                  10                  15
Lys Asp Lys Gly Lys Arg Gly Lys Val Lys Asn Val Leu Ser Ser Gly
            20                  25                  30
Lys Val Ile Val Glu Gly Ile Asn Leu Val Lys Lys His Gln Lys Pro
        35                  40                  45
Val Pro Ala Leu Asn Gln Pro Gly Gly Ile Val Glu Lys Glu Ala Ala
    50                  55                  60
Ile Gln Val Ser Asn Val Ala Ile Phe Asn Ala Ala Thr Gly Lys Ala
65                  70                  75                  80
Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe
                85                  90                  95
Lys Ser Asn Ser Glu Thr Ile Lys
            100
```

<210> [illegible]
<211> 123
<212> PRT
<213> E. Coli

<400> [illegible]

```
Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala
 1               5                  10                  15
Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr
            20                  25                  30
Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro
        35                  40                  45
Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg
    50                  55                  60
Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp
65                  70                  75                  80
Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
                85                  90                  95
Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
            100                 105                 110
Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu
        115                 120
```

<210> 323
<211> 198
<212> PRT
<213> E. Coli

<400> 323

Met Phe Lys Gly Gln Lys Thr Leu Ala Ala Leu Ala Val Ser Leu Leu
1 5 10 15
Phe Thr Ala Pro Val Tyr Ala Ala Asp Glu Gly Ser Gly Glu Ile His
20 25 30
Phe Lys Gly Glu Val Ile Glu Ala Pro Cys Glu Ile His Pro Glu Asp
35 40 45
Ile Asp Lys Asn Ile Asp Leu Gly Gln Val Thr Thr Thr His Ile Asn
50 55 60
Arg Glu His His Ser Asn Lys Val Ala Val Asp Ile Arg Leu Ile Asn
65 70 75 80
Cys Asp Leu Pro Ala Ser Asp Asn Gly Ser Gly Met Pro Val Ser Lys
85 90 95
Val Gly Val Thr Phe Asp Ser Thr Ala Lys Thr Thr Gly Ala Thr Pro
100 105 110
Leu Leu Ser Asn Thr Ser Ala Gly Glu Ala Thr Gly Val Gly Val Arg
115 120 125
Leu Met Asp Lys Asn Asp Gly Asn Ile Val Leu Gly Ser Ala Ala Pro
130 135 140
Asp Leu Asp Leu Asp Ala Ser Ser Ser Glu Gln Thr Leu Asn Phe Phe
145 150 155 160
Ala Trp Met Glu Gln Ile Asp Asn Ala Val Asp Val Thr Ala Gly Glu
165 170 175
Val Thr Ala Asn Ala Thr Tyr Val Leu Asp Tyr Lys
180 185

<210> 324
<211> 437
<212> PRT
<213> E. Coli

<400> 324

Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val
1 5 10 15
Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile
20 25 30
Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr
35 40 45
Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu
50 55 60
Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp
65 70 75 80
Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro
85 90 95
Thr Gln Glu Gln Tyr Asp Glu Phe Lys Thr Thr Val Thr Arg His Thr
100 105 110
Met Ile His Glu Gln Ile Thr Arg Leu Phe His Ala Phe Arg Arg Asp
115 120 125
Ser His Pro Met Ala Val Met Cys Gly Ile Thr Gly Ala Leu Ala Ala
130 135 140
Phe Tyr His Asp Ser Leu Asp Val Asn Asn Pro Arg His Arg Glu Ile

```
145                 150                 155                 160
Ala Ala Phe Arg Leu Leu Ser Lys Met Pro Thr Met Ala Ala Met Cys
                165                 170                 175
Tyr Lys Tyr Ser Ile Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu
            180                 185                 190
Ser Tyr Ala Gly Asn Phe Leu Asn Met Met Phe Ser Thr Pro Cys Glu
        195                 200                 205
Pro Tyr Glu Val Asn Pro Ile Leu Glu Arg Ala Met Asp Arg Ile Leu
    210                 215                 220
Ile Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg
225                 230                 235                 240
Thr Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly
                245                 250                 255
Ile Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Ala
            260                 265                 270
Leu Lys Met Leu Glu Gln Ile Ser Ser Val Lys His Ile Pro Glu Phe
        275                 280                 285
Val Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe
    290                 295                 300
Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Thr Val Met Arg
305                 310                 315                 320
Glu Thr Lys His Glu Val Leu Lys Glu Leu Gly Thr Lys Asp Asp Leu
                325                 330                 335
Leu Glu Val Ala Met Glu Leu Glu Asn Ile Ala Leu Asn Asp Pro Tyr
            340                 345                 350
Phe Ile Glu Lys Lys Leu Tyr Pro Asn Val Asp Phe Tyr Ser Gly Ile
        355                 360                 365
Ile Leu Lys Ala Met Gly Ile Pro Ser Ser Met Phe Thr Val Ile Phe
    370                 375                 380
Ala Met Ala Arg Thr Val Gly Trp Ile Ala His Trp Ser Glu Met His
385                 390                 395                 400
Ser Asp Gly Met Lys Ile Ala Arg Pro Arg Gln Leu Tyr Thr Gly Tyr
                405                 410                 415
Glu Lys Arg Asp Phe Lys Ser Asp Ile Lys Arg
            420                 425
```

Asn Gln Gln Leu Ile Arg Leu Asp Phe Glu Glu Gly Phe Glu Gly Val
115 120 125
Asp Pro Gln Pro Leu His Glu Arg Ile Asn Gln Ala Leu Ser Ser Ile
130 135 140
Gly Ala Leu Val Leu Ser Asp Tyr Ala Lys Gly Ala Leu Ala Ser Val
145 150 155 160
Gln Gln Met Ile Gln Leu Ala Arg Lys Ala Gly Val Pro Val Leu Ile
165 170 175
Asp Pro Lys Gly Thr Asp Phe Glu Arg Tyr Arg Gly Ala Thr Leu Leu
180 185 190
Thr Pro Asn Leu Ser Glu Phe Glu Ala Val Val Gly Lys Cys Lys Thr
195 200 205
Glu Glu Glu Ile Val Glu Arg Gly Met Lys Leu Ile Ala Asp Tyr Glu
210 215 220
Leu Ser Ala Leu Leu Val Thr Arg Ser Glu Gln Gly Met Ser Leu Leu
225 230 235 240
Gln Pro Gly Lys Ala Pro Leu His Met Pro Thr Gln Ala Gln Glu Val
245 250 255
Tyr Asp Val Thr Gly Ala Gly Asp Thr Val Ile Gly Val Leu Ala Ala
260 265 270
Thr Leu Ala Ala Gly Asn Ser Leu Glu Glu Ala Cys Phe Phe Ala Asn
275 280 285
Ala Ala Ala Gly Val Val Val Gly Lys Leu Gly Thr Ser Thr Val Ser
290 295 300
Pro Ile Glu Leu Glu Asn Ala Val Arg Gly Arg Ala Asp Thr Gly Phe
305 310 315 320
Gly Val Met Thr Glu Glu Glu Leu Lys Leu Ala Val Ala Ala Ala Arg
325 330 335
Lys Asn Gly Glu Lys Val Val Met Thr Asn Gly Val Phe Asp Ile Leu
340 345 350
His Ala Gly His Val Ser Tyr Leu Ala Asn Ala Arg Lys Leu Gly Asp
355 360 365
Arg Leu Ile Val Ala Val Asn Ser Asp Ala Ser Thr Lys Arg Leu Lys
370 375 380
Gly Asp Ser Arg Pro Val Asn Pro Leu Glu Gln Arg Met Ile Val Leu
385 390 395 400
Gly Ala Leu Glu Ala Val Asp Trp Val Val Ser Phe Glu Glu Asp Thr
405 410 415
Pro Gln Arg Leu Ile Ala Gly Ile Leu Pro Asp Leu Leu Val Lys Gly
420 425 430
Gly Asp Tyr Lys Pro Glu Glu Ile Ala Gly Ser Lys Glu Val Trp Ala
435 440 445
Asn Gly Gly Glu Val Leu Val Leu Asn Phe Glu Asp Gly Cys Ser Thr
450 455 460
Thr Asn Ile Ile Lys Lys Ile Gln Gln Asp Lys Lys Gly
465 470 475

<210> 316
<211> 946
<212> PRT
<213> E. Coli

<400> 326
Met Lys Pro Leu Ser Ser Pro Leu Gln Gln Tyr Trp Gln Thr Val Val
1 5 10 15
Glu Arg Leu Pro Glu Pro Leu Ala Glu Glu Ser Leu Ser Ala Gln Ala

```
                20                  25                  30
Lys Ser Val Leu Thr Phe Ser Asp Phe Val Gln Asp Ser Val Ile Ala
        35                  40                  45
His Pro Glu Trp Leu Thr Glu Leu Glu Ser Gln Pro Pro Gln Ala Asp
    50                  55                  60
Glu Trp Gln His Tyr Ala Ala Trp Leu Gln Glu Ala Leu Cys Asn Val
65                  70                  75                  80
Ser Asp Glu Ala Gly Leu Met Arg Glu Leu Arg Leu Phe Arg Arg Arg
                85                  90                  95
Ile Met Val Arg Ile Ala Trp Ala Glu Thr Leu Ala Leu Val Thr Glu
            100                 105                 110
Glu Ser Ile Leu Gln Gln Leu Ser Tyr Leu Ala Glu Thr Leu Ile Val
        115                 120                 125
Ala Ala Arg Asp Trp Leu Tyr Asp Ala Cys Cys Arg Glu Trp Gly Thr
    130                 135                 140
Pro Cys Asn Ala Gln Gly Glu Ala Gln Pro Leu Leu Ile Leu Gly Met
145                 150                 155                 160
Gly Lys Leu Gly Gly Gly Glu Leu Asn Phe Ser Ser Asp Ile Asp Leu
                165                 170                 175
Ile Phe Ala Trp Pro Glu His Gly Cys Thr Gln Gly Gly Arg Arg Glu
            180                 185                 190
Leu Asp Asn Ala Gln Phe Phe Thr Arg Met Gly Gln Arg Leu Ile Lys
        195                 200                 205
Val Leu Asp Gln Pro Thr Gln Asp Gly Phe Val Tyr Arg Val Asp Met
    210                 215                 220
Arg Leu Arg Pro Phe Gly Glu Ser Gly Pro Leu Val Leu Ser Phe Ala
225                 230                 235                 240
Ala Leu Glu Asp Tyr Tyr Gln Glu Gln Gly Arg Asp Trp Glu Arg Tyr
                245                 250                 255
Ala Met Val Lys Ala Arg Ile Met Gly Asp Ser Glu Gly Val Tyr Ala
            260                 265                 270
Asn Gln Leu Arg Ala Met Leu Arg Pro Phe Val Phe Arg Arg Tyr Ile
        275                 280                 285
Asp Phe Ser Val Ile Gln Ser Leu Arg Asn Met Lys Gly Met Ile Ala
    290                 295                 300
Arg Glu Val Arg Arg Arg Gly Leu Thr Asp Asn Ile Lys Leu Gly Ala
305                 310                 315                 320
Gly Gly Ile Arg Glu Ile Glu Phe Ile Val Gln Val Phe Gln Leu Ile
                325                 330                 335
Arg Gly Gly Arg Glu Pro Ser Leu Gln Ser Arg Ser Leu Leu Lys Thr
            340                 345                 350
Leu Ser Ala Ile Ala Glu Leu His Leu Leu Ser Glu Asn Asp Ala Glu
        355                 360                 365
Gln Leu Arg Val Ala Tyr Leu Phe Leu Arg Arg Leu Glu Asn Leu Leu
    370                 375                 380
Gln Ser Ile Asn Asp Glu Gln Thr Gln Thr Leu Pro Ser Asp Glu Leu
385                 390                 395                 400
Asn Arg Ala Arg Leu Ala Trp Ala Met Asp Phe Ala Asp Trp Pro Gln
                405                 410                 415
Leu Thr Gly Ala Leu Thr Ala His Met Thr Asn Val Arg Arg Val Phe
            420                 425                 430
Asn Gln Leu Ile Gly Asp Asp Glu Ser Glu Thr Gln Glu Glu Ser Leu
        435                 440                 445
Ser Gln Gln Trp Arg Glu Leu Trp Gln Asp Ala Leu Gln Glu Asp Asp
    450                 455                 460
Thr Thr Pro Val Leu Ala His Leu Ser Glu Asp Asp Arg Lys Gln Val
465                 470                 475                 480
```

Leu Thr Leu Ile Ala Asp Phe Arg Lys Glu Leu Asp Lys Arg Thr Ile
485 490 495
Gly Pro Arg Gly Arg Gln Val Leu Asp His Leu Met Pro His Leu Leu
500 505 510
Ser Asp Val Cys Ala Arg Glu Asp Ala Ala Val Thr Leu Ser Arg Ile
515 520 525
Thr Ala Leu Leu Val Gly Ile Val Thr Arg Thr Thr Tyr Leu Glu Leu
530 535 540
Leu Ser Glu Phe Pro Ala Ala Leu Lys His Leu Ile Ser Leu Cys Ala
545 550 555 560
Ala Ser Pro Met Ile Ala Ser Gln Leu Ala Arg Tyr Pro Leu Leu Leu
565 570 575
Asp Glu Leu Leu Asp Pro Asn Thr Leu Thr Tyr Gln Pro Thr Ala Thr Asp
580 585 590
Ala Tyr Arg Asp Glu Leu Arg Gln Tyr Leu Leu Arg Val Pro Glu Asp
595 600 605
Asp Glu Glu Gln Gln Leu Glu Ala Leu Arg Gln Phe Lys Gln Ala Gln
610 615 620
Leu Leu Arg Ile Ala Ala Ala Asp Ile Ala Gly Thr Leu Pro Val Met
625 630 635 640
Lys Val Ser Asp His Leu Thr Trp Leu Ala Glu Ala Met Ile Asp Ala
645 650 655
Val Val Gln Gln Ala Trp Val Gln Met Val Ala Arg Tyr Gly Lys Pro
660 665 670
Asn His Leu Asn Glu Arg Glu Gly Arg Gly Phe Ala Val Val Gly Tyr
675 680 685
Gly Lys Leu Gly Gly Trp Glu Leu Gly Tyr Ser Ser Asp Leu Asp Leu
690 695 700
Ile Phe Leu His Asp Cys Pro Met Asp Ala Met Thr Asp Gly Glu Arg
705 710 715 720
Glu Ile Asp Gly Arg Gln Phe Tyr Leu Arg Leu Ala Gln Arg Ile Met
725 730 735
His Leu Phe Ser Thr Arg Thr Ser Ser Gly Ile Leu Tyr Glu Val Asp
740 745 750
Ala Arg Leu Arg Pro Ser Gly Ala Ala Gly Met Leu Val Thr Ser Ala
755 760 765
Glu Ala Phe Ala Asp Tyr Gln Lys Asn Glu Ala Trp Thr Trp Glu His
770 775 780
Gln Ala Leu Val Arg Ala Arg Val Val Tyr Gly Asp Pro Gln Leu Thr
785 790 795 800
Ala His Phe Asp Ala Val Arg Arg Glu Ile Met Thr Leu Pro Arg Glu
805 810 815
Gly Lys Thr Leu Gln Thr Glu Val Arg Glu Met Arg Glu Lys Met Arg
820 825 830
Ala His Leu Gly Asn Lys His Arg Asp Arg Phe Asp Ile Lys Ala Asp
835 840 845
Glu Gly Gly Ile Thr Asp Ile Glu Phe Ile Thr Gln Tyr Leu Val Leu
850 855 860
Arg Tyr Ala His Glu Lys Pro Lys Leu Thr Arg Trp Ser Asp Asn Val
865 870 875 880
Arg Ile Leu Gln Leu Leu Ala Gln Asn Asp Ile Met Glu Glu Gln Glu
885 890 895
Ala Met Ala Leu Thr Arg Ala Tyr Thr Thr Leu Arg Asp Glu Leu His
900 905 910
His Leu Ala Leu Gln Glu Leu Pro Gly His Val Ser Glu Asp Cys Phe
915 920 925
Thr Ala Glu Arg Glu Leu Val Arg Ala Ser Trp Gln Lys Trp Leu Val

930 935 940
Glu Glu
945

<210> 327
<211> 443
<212> PRT
<213> E. Coli

<400> 327
Met Ala Gln Glu Ile Glu Leu Lys Phe Ile Val Asn His Ser Ala Val
1 5 10 15
Glu Ala Leu Arg Asp His Leu Asn Thr Leu Gly Gly Glu His His Asp
20 25 30
Pro Val Gln Leu Leu Asn Ile Tyr Tyr Glu Thr Pro Asp Asn Trp Leu
35 40 45
Arg Gly His Asp Met Gly Leu Arg Ile Arg Gly Glu Asn Gly Arg Tyr
50 55 60
Glu Met Thr Met Lys Val Ala Gly Arg Val Thr Gly Gly Leu His Gln
65 70 75 80
Arg Pro Glu Tyr Asn Val Ala Leu Ser Glu Pro Thr Leu Asp Leu Ala
85 90 95
Gln Leu Pro Thr Glu Val Trp Pro Asn Gly Glu Leu Pro Ala Asp Leu
100 105 110
Ala Ser Arg Val Gln Pro Leu Phe Ser Thr Asp Phe Tyr Arg Glu Lys
115 120 125
Trp Leu Val Ala Val Asp Gly Ser Gln Ile Glu Ile Ala Leu Asp Gln
130 135 140
Gly Glu Val Lys Ala Gly Glu Phe Ala Glu Pro Ile Cys Glu Leu Glu
145 150 155 160
Leu Glu Leu Leu Ser Gly Asp Thr Arg Ala Val Leu Lys Leu Ala Asn
165 170 175
Gln Leu Val Ser Gln Thr Gly Leu Arg Gln Gly Ser Leu Ser Lys Ala
180 185 190
Ala Arg Gly Tyr His Leu Ala Gln Gly Asn Pro Ala Arg Glu Ile Lys
195 200 205
Pro Thr Thr Ile Leu His Val Ala Ala Lys Ala Asp Val Glu Gln Gly
210 215 220
Leu Glu Ala Ala Leu Glu Leu Ala Leu Ala Gln Trp Gln Tyr His Glu
225 230 235 240
Glu Leu Trp Val Arg Gly Asn Asp Ala Ala Lys Glu Gln Val Leu Ala
245 250 255
Ala Ile Ser Leu Val Arg His Thr Leu Met Leu Phe Gly Gly Ile Val
260 265 270
Pro Arg Lys Ala Ser Thr His Leu Arg Asp Leu Leu Thr Gln Cys Glu
275 280 285
Ala Thr Ile Ala Ser Ala Val Ser Ala Val Thr Ala Val Tyr Ser Thr
290 295 300
Glu Thr Ala Met Ala Lys Leu Ala Leu Thr Glu Trp Leu Val Ser Lys
305 310 315 320
Ala Trp Gln Pro Phe Leu Asp Ala Lys Ala Gln Gly Lys Ile Ser Asp
325 330 335
Ser Phe Lys Arg Phe Ala Asp Ile His Leu Ser Arg His Ala Ala Glu
340 345 350
Leu Lys Ser Val Phe Cys Gln Pro Leu Gly Asp Arg Tyr Arg Asp Gln

```
        355                 360                 365
Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Leu Ala Gly
    370                 375                 380
Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly
385                 390                 395                 400
Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe
                405                 410                 415
Arg Asn Gln Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys
            420                 425                 430
Arg
```


(210) 328
(211) 70
(212) PRT
(213) E. Coli

(400) 328
Met Ser Gly Lys Met Thr Gly Ile Val Lys Trp Phe Asn Ala Asp Lys
 1   5   10   15
Gly Phe Gly Phe Ile Thr Pro Asp Asp Gly Ser Lys Asp Val Phe Val
            20   25   30
His Phe Ser Ala Ile Gln Asn Asp Gly Tyr Lys Ser Leu Asp Glu Gly
        35   40   45
Gln Lys Val Ser Phe Thr Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
    50   55   60
Gly Asn Val Thr Ser Leu
65   70

(210) 329
(211) 113
(212) PRT
(213) E. Coli

(400) 329
Met Arg Asp Ile Val Asp Pro Val Phe Ser Ile Gly Ile Ser Ser Leu
 1   5   10   15
Trp Asp Glu Leu Arg His Met Pro Ala Gly Gly Val Trp Trp Phe Asn
            20   25   30
Val Asp Arg His Glu Asp Ala Ile Ser Leu Ala Asn Gln Thr Ile Ala
        35   40   45
Ser Gln Ala Glu Thr Ala His Val Ala Val Ile Ser Met Asp Ser Asp
    50   55   60
Pro Ala Lys Ile Phe Gln Leu Asp Asp Ser Gln Gly Pro Glu Lys Ile
65   70   75   80
Lys Leu Phe Ser Met Leu Asn His Glu Lys Gly Leu Tyr Tyr Leu Thr
                85   90   95
Arg Asp Leu Gln Cys Ser Ile Asp Pro His Asn Tyr Leu Phe Ile Leu
            100   105   110
Val Cys Ala Asn Asn Ala Trp Gln Asn Ile Pro Ala Glu Arg Leu Arg
        115   120   125
Ser Trp Leu Asp Lys Met Asn Lys Trp Ser Arg Leu Asn His Cys Ser
    130   135   140
```
```

Leu Leu Val Ile Asn Pro Gly Asn Asn Asn Asp Lys Gln Phe Ser Leu
145 150 155 160
Leu Leu Glu Glu Tyr Arg Ser Leu Phe Gly Leu Ala Ser Leu Arg Phe
165 170 175
Gln Gly Asp Gln His Leu Leu Asp Ile Ala Phe Trp Cys Asn Glu Lys
180 185 190
Gly Val Ser Ala Arg Gln Gln Leu Ser Val Gln Gln Gln Asn Gly Ile
195 200 205
Trp Thr Leu Val Gln Ser Glu Glu Ala Glu Ile Gln Pro Arg Ser Asp
210 215 220
Glu Lys Arg Ile Leu Ser Asn Val Ala Val Leu Glu Gly Ala Pro Pro
225 230 235 240
Leu Ser Glu His Trp Gln Leu Phe Asn Asn Glu Val Leu Phe Asn
245 250 255
Glu Ala Arg Thr Ala Gln Ala Ala Thr Val Val Phe Ser Leu Gln Gln
260 265 270
Asn Ala Gln Ile Glu Pro Leu Ala Arg Ser Ile His Thr Leu Arg Arg
275 280 285
Gln Arg Gly Ser Ala Met Lys Ile Leu Val Arg Glu Asn Thr Ala Ser
290 295 300
Leu Arg Ala Thr Asp Glu Arg Leu Leu Leu Ala Cys Gly Ala Asn Met
305 310 315 320
Val Ile Pro Trp Asn Ala Pro Leu Ser Arg Cys Leu Thr Met Ile Glu
325 330 335
Ser Val Gln Gly Gln Lys Phe Ser Arg Tyr Val Pro Glu Asp Ile Thr
340 345 350
Thr Leu Leu Ser Met Thr Gln Pro Leu Lys Leu Arg Gly Phe Gln Lys
355 360 365
Trp Asp Val Phe Cys Asn Ala Val Asn Asn Met Met Asn Asn Pro Leu
370 375 380
Leu Pro Ala His Gly Lys Gly Val Leu Val Ala Leu Arg Pro Val Pro
385 390 395 400
Gly Ile Arg Val Glu Gln Ala Leu Thr Leu Cys Arg Pro Asn Arg Thr
405 410 415
Gly Asp Ile Met Thr Ile Gly Gly Asn Arg Leu Val Leu Phe Leu Ser
420 425 430
Phe Cys Arg Ile Asn Asp Leu Asp Thr Ala Leu Asn His Ile Phe Pro
435 440 445
Leu Pro Thr Gly Asp Ile Phe Ser Asn Arg Met Val Trp Phe Glu Asp
450 455 460
Asp Gln Ile Ser Ala Glu Leu Val Gln Met Arg Leu Leu Ala Pro Glu
465 470 475 480
Gln Trp Gly Met Pro Leu Pro Leu Thr Gln Ser Ser Lys Pro Val Ile
485 490 495
Asn Ala Glu His Asp Gly Arg His Trp Arg Arg Ile Pro Glu Pro Met
500 505 510
Arg Leu Leu Asp Asp Ala Val Glu Arg Ser Ser
515 520

<210> 330
<211> 62
<212> PRT
<213> E. Coli

<400> 330
Met Thr Ile Ser Asp Ile Ile Glu Ile Ile Val Val Cys Ala Leu Ile

1 5 10 15
Phe Phe Pro Leu Gly Tyr Leu Ala Arg His Ser Leu Arg Arg Ile Arg
20 25 30
Asp Thr Leu Arg Leu Phe Phe Ala Lys Pro Arg Tyr Val Lys Pro Ala
35 40 45
Gly Thr Leu Arg Arg Thr Glu Lys Ala Arg Ala Thr Lys Lys
50 55 60

<210> 331
<211> 339
<212> DNA
<213> E. Coli

<400> 331
Met Thr Gln Phe Thr Gln Asn Thr Ala Met Pro Ser Ser Leu Trp Gln
1 5 10 15
Tyr Trp Arg Gly Leu Ser Gly Trp Asn Phe Tyr Phe Leu Val Lys Phe
20 25 30
Gly Leu Leu Trp Ala Gly Tyr Leu Asn Phe His Pro Leu Leu Asn Leu
35 40 45
Val Phe Ala Ala Phe Leu Leu Met Pro Leu Pro Arg Tyr Ser Leu His
50 55 60
Arg Leu Arg His Trp Ile Ala Leu Pro Ile Gly Phe Ala Leu Phe Trp
65 70 75 80
His Asp Thr Trp Leu Pro Gly Pro Glu Ser Ile Met Ser Gln Gly Ser
85 90 95
Gln Val Ala Gly Phe Ser Thr Asp Tyr Leu Ile Asp Leu Val Thr Arg
100 105 110
Phe Ile Asn Trp Gln Met Ile Gly Ala Ile Phe Val Leu Leu Val Ala
115 120 125
Trp Leu Phe Leu Ser Gln Trp Ile Arg Ile Thr Val Phe Val Val Ala
130 135 140
Ile Leu Leu Trp Leu Asn Val Leu Thr Leu Ala Gly Pro Ser Phe Ser
145 150 155 160
Leu Trp Pro Ala Gly Gln Pro Thr Thr Thr Val Thr Thr Thr Gly Gly
165 170 175
Asn Ala Ala Ala Thr Val Ala Ala Thr Gly Gly Ala Pro Val Val Gly
180 185 190
Asp Met Pro Ala Gln Thr Ala Pro Pro Thr Thr Ala Asn Leu Asn Ala
195 200 205
Trp Leu Asn Asn Phe Tyr Asn Ala Glu Ala Lys Arg Lys Ser Thr Phe
210 215 220
Pro Ser Ser Leu Pro Ala Asp Ala Gln Pro Phe Glu Leu Leu Val Ile
225 230 235 240
Asn Ile Cys Ser Leu Ser Trp Ser Asp Ile Glu Ala Ala Gly Leu Met
245 250 255
Ser His Pro Leu Trp Ser His Phe Asp Ile Glu Phe Lys Asn Phe Asn
260 265 270
Ser Ala Thr Ser Tyr Ser Gly Pro Ala Ala Ile Arg Leu Leu Arg Ala
275 280 285
Ser Cys Gly Gln Thr Ser His Thr Asn Leu Tyr Gln Pro Ala Asn Asn
290 295 300
Asp Cys Tyr Leu Phe Asp Asn Leu Ser Lys Leu Gly Phe Thr Gln His
305 310 315 320
Leu Met Met Gly His Asn Gly Gln Phe Gly Gly Phe Leu Lys Glu Val
325 330 335

Arg Glu Asn Gly Gly Met Gln Ser Glu Leu Met Asp Gln Thr Asn Leu
340 345 350
Pro Val Ile Leu Leu Gly Phe Asp Gly Ser Pro Val Tyr Asp Asp Thr
355 360 365
Ala Val Leu Asn Arg Trp Leu Asp Val Thr Glu Lys Asp Lys Asn Ser
370 375 380
Arg Ser Ala Thr Phe Tyr Asn Thr Leu Pro Leu His Asp Gly Asn His
385 390 395 400
Tyr Pro Gly Val Ser Lys Thr Ala Asp Tyr Lys Ala Arg Ala Gln Lys
405 410 415
Phe Phe Asp Glu Leu Asp Ala Phe Phe Thr Glu Leu Glu Lys Ser Gly
420 425 430
Arg Lys Val Met Val Val Val Val Pro Glu His Gly Gly Ala Leu Lys
435 440 445
Gly Asp Arg Met Gln Val Ser Gly Leu Arg Asp Ile Pro Ser Pro Ser
450 455 460
Ile Thr Asp Val Pro Val Gly Val Lys Phe Phe Gly Met Lys Ala Pro
465 470 475 480
His Gln Gly Ala Pro Ile Val Ile Glu Gln Pro Ser Ser Phe Leu Ala
485 490 495
Ile Ser Asp Leu Val Val Arg Val Leu Asp Gly Lys Ile Phe Thr Glu
500 505 510
Asp Asn Val Asp Trp Lys Lys Leu Thr Ser Gly Leu Pro Gln Thr Ala
515 520 525
Pro Val Ser Glu Asn Ser Asn Ala Val Val Ile Gln Tyr Gln Asp Lys
530 535 540
Pro Tyr Val Arg Leu Asn Gly Gly Asp Trp Val Pro Tyr Pro Gln
545 550 555

<210> 37
<211> 127
<212> PRT
<213> E. Coli

<400> 37
Met Gln Gly Ser Arg Met Lys Tyr Arg Ile Ala Leu Ala Val Ser Leu
1 5 10 15
Phe Ala Leu Ser Ala Gly Ser Tyr Ala Thr Thr Leu Cys Gln Glu Lys
20 25 30
Glu Gln Asn Ile Leu Lys Glu Ile Ser Tyr Ala Glu Lys His Gln Asn
35 40 45
Gln Asn Arg Ile Asp Gly Leu Asn Lys Ala Leu Ser Glu Val Arg Ala
50 55 60
Asn Cys Ser Asp Ser Gln Leu Arg Ala Asp His Gln Lys Lys Ile Ala
65 70 75 80
Lys Gln Lys Asp Glu Val Ala Glu Arg Gln Gln Asp Leu Ala Glu Ala
85 90 95
Lys Gln Lys Gly Asp Ala Asp Lys Ile Ala Lys Arg Glu Arg Lys Leu
100 105 110
Ala Glu Ala Gln Glu Glu Leu Lys Lys Leu Glu Ala Arg Asp Tyr
115 120 125

<210> 38
<211> 111
<212> PRT

<213> E. Coli

<400> 333

Met Ser Lys Glu His Thr Thr Glu His Leu Arg Ala Glu Leu Lys Ser
1 5 10 15
Leu Ser Asp Thr Leu Glu Glu Val Leu Ser Ser Ser Gly Glu Lys Ser
20 25 30
Lys Glu Gln Leu Ser Lys Ile Arg Ser Lys Ala Glu Gln Ala Leu Lys
35 40 45
Gln Ser Arg Tyr Arg Leu Gly Glu Thr Gly Asp Ala Ile Ala Lys Gln
50 55 60
Thr Arg Val Ala Ala Ala Arg Ala Asp Glu Tyr Val Arg Glu Asn Pro
65 70 75 80
Trp Thr Gly Val Gly Ile Gly Ala Ala Ile Gly Val Val Leu Gly Val
85 90 95
Leu Leu Ser Arg Arg
100

<210> 334
<211> 136
<212> PRT
<213> E. Coli

<400> 334

Met Ala Asp Thr His His Ala Gln Gly Pro Gly Lys Ser Val Leu Gly
1 5 10 15
Ile Gly Gln Arg Ile Val Ser Ile Met Val Glu Met Val Glu Thr Arg
20 25 30
Leu Arg Leu Ala Val Val Glu Leu Glu Gln Glu Lys Ala Asn Leu Phe
35 40 45
Gln Leu Leu Leu Met Leu Gly Leu Thr Met Leu Phe Ala Ala Phe Gly
50 55 60
Leu Met Ser Leu Met Val Leu Ile Ile Trp Ala Val Asp Pro Gln Tyr
65 70 75 80
Arg Leu Asn Ala Met Ile Ala Thr Thr Val Val Leu Leu Leu Leu Ala
85 90 95
Leu Ile Gly Gly Ile Trp Thr Leu Arg Lys Ser Arg Lys Ser Thr Leu
100 105 110
Leu Arg His Thr Arg His Glu Leu Ala Asn Asp Arg Gln Leu Leu Glu
115 120 125
Glu Gln Ser Arg Glu Gln
130

<210> 335
<211> 99
<212> PRT
<213> E. Coli

<400> 335

Met Ser Ser Lys Val Glu Arg Glu Arg Arg Lys Ala Gln Leu Leu Ser
1 5 10 15
Gln Ile Gln Gln Gln Arg Leu Asp Leu Ser Ala Ser Arg Arg Glu Trp
20 25 30
Leu Glu Thr Thr Gly Ala Tyr Asp Arg Arg Trp Asn Met Leu Leu Ser

```
        35                  40                  45
Leu Arg Ser Trp Ala Leu Val Gly Ser Ser Val Met Ala Ile Trp Thr
    50                  55                  60
Ile Arg His Pro Asn Met Leu Val Arg Trp Ala Arg Arg Gly Phe Gly
65                  70                  75                  80
Val Trp Ser Ala Trp Arg Leu Val Lys Thr Thr Leu Lys Gln Gln Gln
                85                  90                  95
Leu Arg Gly
```

(210) 136

(211) 160

(212) PRT

(213) E. Coli

(400) 136

```
Met Ile Leu Ser Ile Asp Ser Asn Asp Ala Asn Thr Ala Pro Leu His
 1               5                  10                  15
Lys Lys Thr Leu Ser Ser Leu Ser Gly Ala Val Glu Ser Met Met Lys
            20                  25                  30
Lys Leu Gln Asp Val Gly Val Leu Val Ala Arg Ile Leu Met Pro Ile
        35                  40                  45
Leu Phe Ile Thr Ala Gly Trp Gly Lys Ile Thr Gly Tyr Ala Gly Thr
    50                  55                  60
Gln Gln Tyr Met Glu Ala Met Gly Val Pro Gly Phe Met Leu Pro Leu
65                  70                  75                  80
Val Ile Leu Leu Leu Glu Phe Gly Gly Gly Leu Ala Ile Leu Phe Gly Phe
                85                  90                  95
Leu Thr Arg Thr Thr Ala Leu Phe Thr Ala Gly Phe Thr Leu Leu Thr
            100                 105                 110
Ala Phe Leu Phe His Ser Asn Phe Ala Glu Gly Val Asn Ser Leu Met
        115                 120                 125
Phe Met Lys Asn Leu Thr Ile Ser Gly Gly Phe Leu Leu Leu Ala Ile
    130                 135                 140
Thr Gly Pro Gly Ala Tyr Ser Ile Asp Arg Leu Leu Asn Lys Lys Trp
145                 150                 155                 160
```

(210) 337

(211) 146

(212) PRT

(213) E. Coli

(400) 337

```
Met Ile Lys Lys Thr Thr Glu Ile Asp Ala Ile Leu Leu Asn Leu Asn
 1               5                  10                  15
Lys Ala Ile Asp Ala His Tyr Gln Trp Leu Val Ser Met Phe His Ser
            20                  25                  30
Val Val Ala Arg Asp Ala Ser Lys Pro Glu Ile Thr Asp Asn His Ser
        35                  40                  45
Tyr Gly Leu Cys Gln Phe Gly Arg Trp Ile Asp His Leu Gly Pro Leu
    50                  55                  60
Asp Asn Asp Glu Leu Pro Tyr Val Arg Leu Met Asp Ser Ala His Gln
65                  70                  75                  80
```

His Met His Asn Cys Gly Arg Glu Leu Met Leu Ala Ile Val Glu Asn
85 90 95
His Trp Gln Asp Ala His Phe Asp Ala Phe Gln Glu Gly Leu Leu Ser
100 105 110
Phe Thr Ala Ala Leu Thr Asp Tyr Lys Ile Tyr Leu Leu Thr Ile Arg
115 120 125
Ser Asn Met Asp Val Leu Thr Gly Leu Pro Gly Arg Arg Val Leu Asp
130 135 140
Glu Ser Phe Asp His Gln Leu Arg Asn Ala Glu Pro Leu Asn Leu Tyr
145 150 155 160
Leu Met Leu Leu Asp Ile Asp Arg Phe Lys Leu Val Asn Asp Thr Tyr
165 170 175
Gly His Leu Ile Gly Asp Val Val Leu Arg Thr Leu Ala Thr Tyr Leu
180 185 190
Ala Ser Trp Thr Arg Asp Tyr Glu Thr Val Tyr Arg Tyr Gly Gly Glu
195 200 205
Glu Phe Ile Ile Ile Val Lys Ala Ala Asn Asp Glu Glu Ala Cys Arg
210 215 220
Ala Gly Val Arg Ile Cys Gln Leu Val Asp Asn His Ala Ile Thr His
225 230 235 240
Ser Gln Gly His Ile Asn Ile Thr Val Thr Ala Gly Val Ser Arg Ala
245 250 255
Phe Pro Glu Glu Pro Leu Asp Val Val Ile Gly Arg Ala Asp Arg Ala
260 265 270
Met Tyr Glu Gly Lys Gln Thr Gly Arg Asn Arg Cys Met Phe Ile Asp
275 280 285
Glu Gln Asn Val Ile Asn Arg Val
290 295

<210> 56
<211> 20
<212> PRT
<213> E. Coli

<400> 56
Met Arg Leu Asn Val Val Pro Gly Phe Ile Ser Pro Pro Pro Gly Phe
1 5 10 15
Gly Gly Leu Gly Tyr Thr Pro Thr Ala Arg Ala Cys Val Asn Ile Ser
20 25 30
Ile Pro Leu Gln Leu Arg Val Ile Asp Met Leu Asp Val Phe Thr Pro
35 40 45
Leu Leu Lys Leu Phe Ala Asn Glu Pro Leu Glu Arg Leu Met Tyr Thr
50 55 60
Ile Ile Ile Phe Gly Leu Thr Leu Trp Leu Ile Pro Lys Glu Phe Thr
65 70 75 80
Val Ala Phe Asn Ala Tyr Thr Glu Ile Pro Trp Leu Phe Gln Ile Ile
85 90 95
Val Phe Ala Phe Ser Phe Val Val Ala Ile Ser Phe Ser Arg Leu Arg
100 105 110
Ala His Ile Gln Lys His Tyr Ser Leu Leu Pro Glu Gln Arg Val Leu
115 120 125
Leu Arg Leu Ser Glu Lys Glu Ile Ala Val Phe Lys Asp Phe Leu Lys
130 135 140
Thr Gly Asn Leu Ile Ile Thr Ser Pro Cys Arg Asn Pro Val Met Lys
145 150 155 160

Lys Leu Glu Arg Lys Gly Ile Ile Gln His Gln Ser Asp Ser Ala Asn
165 170 175
Cys Ser Tyr Tyr Leu Val Thr Glu Lys Tyr Ser His Phe Met Lys Leu
180 185 190
Phe Trp Asn Ser Arg Ser Arg Arg Phe Asn Arg
195 200

(211) 549
(211) bp
(212) DNA
(213) E. Coli

(400) 549
Met Leu Leu Gln Pro Ser Ala Arg Thr Ser Phe Gly Phe Lys Cys Phe
1 5 10 15
Ala Phe Gly Ile Arg His Gly Ser Glu Arg Ser Ile Leu Val Gly Glu
20 25 30
His Ala Ala His Gln Gly Phe Val Val Ala Glu Val Asp Phe Leu His
35 40 45
Phe Ala Asn Leu Thr Ser Cys Cys Tyr Val
50 55

(210) 941
(211) 1426
(212) DNA
(213) E. Coli

(400) 941
Met Ser Gly Lys Pro Ala Ala Arg Gln Gly Asp Met Thr Gln Tyr Gly
1 5 10 15
Gly Pro Ile Val Gln Gly Ser Ala Gly Val Arg Ile Gly Ala Pro Thr
20 25 30
Gly Val Ala Cys Ser Val Cys Pro Gly Gly Met Thr Ser Gly Asn Pro
35 40 45
Val Asn Pro Leu Leu Gly Ala Lys Val Leu Pro Gly Glu Thr Asp Leu
50 55 60
Ala Leu Pro Gly Pro Leu Pro Phe Ile Leu Ser Arg Thr Tyr Ser Ser
65 70 75 80
Tyr Arg Thr Lys Thr Pro Ala Pro Val Gly Val Phe Gly Pro Gly Trp
85 90 95
Lys Ala Pro Ser Asp Ile Arg Leu Gln Leu Arg Asp Asp Gly Leu Ile
100 105 110
Leu Asn Asp Asn Gly Gly Arg Ser Ile His Phe Glu Pro Leu Leu Pro
115 120 125
Gly Glu Ala Val Tyr Ser Arg Ser Glu Ser Met Trp Leu Val Arg Gly
130 135 140
Gly Lys Ala Ala Gln Pro Asp Gly His Thr Leu Ala Arg Leu Trp Gly
145 150 155 160
Ala Leu Pro Pro Asp Ile Arg Leu Ser Pro His Leu Tyr Leu Ala Thr
165 170 175
Asn Ser Ala Gln Gly Pro Trp Trp Ile Leu Gly Trp Ser Glu Arg Val
180 185 190
Pro Gly Ala Glu Asp Val Leu Pro Ala Pro Leu Pro Pro Tyr Arg Val
195 200 205

Leu Thr Gly Met Ala Asp Arg Phe Gly Arg Thr Leu Thr Tyr Arg Arg
210 215 220
Glu Ala Ala Gly Asp Leu Ala Gly Glu Ile Thr Gly Val Thr Asp Gly
225 230 235 240
Ala Gly Arg Glu Phe Arg Leu Val Leu Thr Thr Gln Ala Gln Arg Ala
245 250 255
Glu Glu Ala Arg Thr Ser Ser Leu Ser Ser Ser Asp Ser Ser Arg Pro
260 265 270
Leu Ser Ala Ser Ala Phe Pro Asp Thr Leu Pro Gly Thr Glu Tyr Gly
275 280 285
Pro Asp Arg Gly Ile Arg Leu Ser Ala Val Trp Leu Met His Asp Pro
290 295 300
Ala Tyr Pro Glu Ser Leu Pro Ala Ala Pro Leu Val Arg Tyr Thr Tyr
305 310 315 320
Thr Gln Ala Gly Glu Leu Leu Ala Val Tyr Asp Arg Ser Asn Thr Gln
325 330 335
Val Arg Ala Phe Thr Tyr Asp Ala Gln His Pro Gly Arg Met Val Ala
340 345 350
His Arg Tyr Ala Gly Arg Pro Glu Met Arg Tyr Arg Tyr Asp Asp Thr
355 360 365
Gly Arg Val Val Glu Gln Leu Asn Pro Ala Gly Leu Ser Tyr Arg Tyr
370 375 380
Leu Tyr Glu Gln Asp Arg Leu Thr Val Thr Asp Ser Leu Asn Arg Arg
385 390 395 400
Glu Val Leu His Thr Glu Gly Gly Ala Gly Leu Lys Arg Val Val Lys
405 410 415
Lys Thr Leu Ala Asp Gly Ser Val Thr Arg Ser Gly Tyr Asp Ala Ala
420 425 430
Gly Arg Leu Thr Ala Gln Thr Asp Ala Ala Gly Arg Thr Glu Tyr
435 440 445
Gly Leu Asn Val Val Ser Gly Asp Ile Thr Asp Leu Thr Thr Pro Asp
450 455 460
Gly Arg Glu Thr Lys Phe Tyr Tyr Asn Asp Gly Asn Gln Leu Thr Ala
465 470 475 480
Val Val Ser Pro Asp Gly Leu Glu Ser Arg Arg Gln Tyr Asp Glu Pro
485 490 495
Gly Arg Leu Val Ser Glu Thr Ser Arg Ser Gly Gln Thr Val Arg Tyr
500 505 510
Arg Tyr Asp Asp Ala His Ser Glu Leu Pro Ala Thr Thr Thr Asp Ala
515 520 525
Thr Gly Ser Thr Arg Gln Met Thr Trp Ser Arg Tyr Gly Gln Leu Leu
530 535 540
Ala Phe Thr Asp Cys Ser Gly Tyr Gln Thr Arg Tyr Glu Tyr Asp Arg
545 550 555 560
Phe Gly Gln Met Thr Ala Val His Arg Glu Gln Gly Ile Ser Leu Tyr
565 570 575
Arg Arg Tyr Asp Asn Arg Gly Arg Leu Thr Ser Val Lys Asp Ala Gln
580 585 590
Gly Arg Glu Thr Arg Tyr Gln Tyr Asn Ala Ala Gly Asp Leu Thr Ala
595 600 605
Val Ile Thr Pro Asp Gly Asn Arg Ser Glu Thr Gln Tyr Asp Ala Trp
610 615 620
Gly Lys Ala Val Ser Thr Thr Gln Gly Gly Leu Thr Arg Ser Met Glu
625 630 635 640
Tyr Asp Ala Ala Gly Arg Val Ile Ser Leu Thr Asn Glu Asn Gly Ser
645 650 655
His Ser Val Phe Ser Tyr Asp Ala Leu Asp Arg Leu Val Gln Gln Gly

Gly Phe Asp Gly Arg Thr Gln Arg Tyr His Tyr Asp Leu Thr Gly Lys
Leu Thr Gln Ser Glu Asp Glu Gly Leu Val Ile Leu Trp Tyr Tyr Asp
Glu Ser Asp Asn Ile Thr His Arg Thr Val Asn Gly Glu Pro Ala Glu
Gln Trp Gln Tyr Asp Gly His Gly Trp Leu Thr Asp Ile Ser His Leu
Ser Glu Gly His Arg Val Ala Val His Tyr Gly Tyr Asp Asp Lys Gly
Arg Leu Thr Gly Glu Cys Gln Thr Val Glu Asn Pro Glu Thr Gly Glu
Leu Leu Trp Gln His Glu Thr Lys His Ala Tyr Asn Glu Gln Gly Leu
Ala Asn Arg Val Thr Pro Asp Ser Leu Pro Pro Val Glu Trp Leu Thr
Tyr Gly Ser Gly Tyr Leu Ala Gly Met Lys Leu Gly Gly Thr Pro Leu
Val Glu Tyr Thr Arg Asp Arg Leu His Arg Glu Thr Val Arg Ser Phe
Gly Ser Met Ala Gly Ser Asn Ala Ala Tyr Glu Leu Thr Ser Thr Tyr
Thr Pro Ala Gly Gln Leu Gln Ser Gln His Leu Asn Ser Leu Val Tyr
Asp Arg Asp Tyr Gly Trp Ser Asp Asn Gly Asp Leu Val Arg Ile Ser
Gly Pro Arg Gln Thr Arg Glu Tyr Gly Tyr Ser Ala Thr Gly Arg Leu
Glu Ser Val Arg Thr Leu Ala Pro Asp Leu Asp Ile Arg Ile Pro Tyr
Ala Thr Asp Pro Ala Gly Asn Arg Leu Pro Asp Pro Glu Leu His Pro
Asp Ser Thr Leu Thr Val Trp Pro Asp Asn Arg Ile Ala Glu Asp Ala
His Tyr Val Tyr Arg His Asp Glu Tyr Gly Arg Leu Thr Glu Lys Thr
Asp Arg Ile Pro Ala Gly Val Ile Arg Thr Asp Asp Glu Arg Thr His
His Tyr His Tyr Asp Ser Gln His Arg Leu Val Phe Tyr Thr Arg Ile
Gln His Gly Gln Pro Leu Val Glu Ser Arg Tyr Leu Tyr Asp Pro Leu
Gly Arg Arg Met Ala Lys Arg Val Trp Arg Arg Glu Arg Asp Leu Thr
Gly Trp Met Ser Leu Ser Arg Lys Pro Glu Val Thr Trp Tyr Gly Trp
Asp Gly Asp Arg Leu Thr Thr Val Gln Thr Asp Thr Thr Arg Ile Gln
Thr Val Tyr Glu Pro Gly Ser Phe Thr Pro Leu Ile Arg Val Glu Thr
Glu Asn Gly Glu Arg Glu Lys Ala Gln Arg Arg Ser Leu Ala Glu Thr
Leu Gln Gln Glu Gly Ser Glu Asn Gly His Gly Val Val Phe Pro Ala
Glu Leu Val Arg Leu Leu Asp Arg Leu Glu Glu Glu Ile Arg Ala Asp

Arg Val Ser Ser Glu Ser Arg Ala Trp Leu Ala Gln Cys Gly Leu Thr
1125 1130 1135
Val Glu Gln Leu Ala Arg Gln Val Glu Pro Glu Tyr Thr Pro Ala Arg
1140 1145 1150
Lys Ala His Leu Tyr His Cys Asp His Arg Gly Leu Pro Leu Ala Leu
1155 1160 1165
Ile Ser Glu Asp Gly Asn Thr Ala Trp Ser Ala Glu Tyr Asp Glu Trp
1170 1175 1180
Gly Asn Gln Leu Asn Glu Glu Asn Pro His His Val Tyr Gln Pro Tyr
1185 1190 1195 1200
Arg Leu Pro Gly Gln Gln His Asp Glu Glu Ser Gly Leu Tyr Tyr Asn
1205 1210 1215
Arg His Asn Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr Ile Thr Gln Asp
1220 1225 1230
Pro Met Gly Leu Lys Gly Gly Trp Asn Leu Tyr Gln Tyr Pro Leu Asn
1235 1240 1245
Pro Leu Gln Gln Ile Asp Pro Met Gly Leu Leu Gln Thr Trp Asp Asp
1250 1255 1260
Ala Arg Ser Gly Ala Cys Thr Gly Gly Val Cys Gly Val Leu Ser Arg
1265 1270 1275 1280
Ile Ile Gly Pro Ser Lys Phe Asp Ser Thr Ala Asp Ala Ala Leu Asp
1285 1290 1295
Ala Leu Lys Glu Thr Gln Asn Arg Ser Leu Cys Asn Asp Met Glu Tyr
1300 1305 1310
Ser Gly Ile Val Cys Lys Asp Thr Asn Gly Lys Tyr Phe Ala Ser Lys
1315 1320 1325
Ala Glu Thr Asp Asn Leu Arg Lys Glu Ser Tyr Pro Leu Lys Asp Lys
1330 1335 1340
Cys Pro Thr Gly Thr Asp Arg Val Ala Ala Tyr His Thr His Gly Ala
1345 1350 1355 1360
Asp Ser His Gly Asp Tyr Val Asp Glu Phe Phe Ser Ser Ser Asp Lys
1365 1370 1375
Asn Leu Val Arg Ser Lys Asp Asn Asn Leu Glu Ala Phe Tyr Leu Ala
1380 1385 1390
Thr Pro Asp Gly Arg Phe Glu Ala Leu Asn Asn Lys Gly Glu Tyr Ile
1395 1400 1405
Phe Ile Asn Asn Ser Val Pro Gly Leu Ser Ser Val Cys Ile Pro Tyr
1410 1415 1420
His Asp
1425

<210> 341
<211> 1425
<212> PRT
<213> E. Coli

<400> 341
Met Lys Tyr Ser Ser Ile Phe Ser Met Leu Ser Phe Phe Ile Leu Phe
1 5 10 15
Ala Cys Asn Glu Thr Ala Val Tyr Gly Ser Asp Glu Asn Ile Ile Phe
20 25 30
Met Arg Tyr Val Glu Lys Leu His Leu Asp Lys Tyr Ser Val Lys Asn
35 40 45
Thr Val Lys Thr Glu Thr Met Ala Ile Gln Leu Ala Glu Ile Tyr Val
50 55 60
Arg Tyr Arg Tyr Gly Glu Arg Ile Ala Glu Glu Glu Lys Pro Tyr Leu

65 70 75 80
Ile Thr Glu Leu Pro Asp Ser Trp Val Val Glu Gly Ala Lys Leu Pro
85 90 95
Tyr Glu Val Ala Gly Gly Val Phe Ile Ile Glu Ile Asn Lys Lys Asn
100 105 110
Gly Cys Val Leu Asn Phe Leu His Ser Lys
115 120

<210> 342
<211> 936
<212> DNA
<213> E. Coli

<400> 342
Met Leu Ala Leu Met Asp Ala Asp Gly Asn Ile Ala Trp Ser Gly Glu
1 5 10 15
Tyr Asp Glu Trp Gly Asn Gln Leu Asn Glu Glu Asn Pro His His Leu
20 25 30
His Gln Pro Tyr Arg Leu Pro Gly Gln Gln Tyr Asp Lys Glu Ser Gly
35 40 45
Leu Tyr Tyr Asn Arg Asn Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr
50 55 60
Ile Thr Gln Asp Pro Ile Gly Leu Glu Gly Gly Trp Ser Leu Tyr Ala
65 70 75 80
Tyr Pro Leu Asn Pro Val Asn Gly Ile Asp Pro Leu Gly Leu Ser Pro
85 90 95
Ala Asp Val Ala Leu Ile Arg Arg Lys Asp Gln Leu Asn His Gln Arg
100 105 110
Ala Trp Asp Ile Leu Ser Asp Thr Tyr Glu Asp Met Lys Arg Leu Asn
115 120 125
Leu Gly Gly Thr Asp Gln Phe Phe His Cys Met Ala Phe Cys Arg Val
130 135 140
Ser Lys Leu Asn Asp Ala Gly Val Ser Arg Ser Ala Lys Gly Leu Gly
145 150 155 160
Tyr Glu Lys Glu Ile Arg Asp Tyr Gly Leu Asn Leu Phe Gly Met Tyr
165 170 175
Gly Arg Lys Val Lys Leu Ser His Ser Glu Met Ile Glu Asp Asn Lys
180 185 190
Lys Asp Leu Ala Val Asn Asp His Gly Leu Thr Cys Pro Ser Thr Thr
195 200 205
Asp Cys Ser Asp Arg Cys Ser Asp Tyr Ile Asn Pro Glu His Lys Lys
210 215 220
Thr Ile Lys Ala Leu Gln Asp Ala Gly Tyr Leu Lys
225 230 235

<210> 343
<211> 84
<212> PRT
<213> E. Coli

<400> 343
Met Leu Ala Ile Ser Ser Asn Leu Ser Lys Met Ile Ile Phe Ile Phe
1 5 10 15
Ala Ile Ile Ile Ile Val Val Leu Cys Val Ile Thr Tyr Leu Tyr Leu
20 25 30

Tyr Lys Asp Glu Ser Leu Val Ser Lys His Tyr Ile Asn Tyr Met Ala
35 40 45
Ile Pro Glu Asn Asp Gly Val Phe Thr Trp Leu Pro Asp Phe Phe Pro
50 55 60
His Val Ala Val Asp Ile Ser Ile Tyr Thr Asn Val Glu Asp Asp Tyr
65 70 75 80
Phe Phe Leu Ile Phe Pro
85

<210> 344
<211> 89
<212> PRT
<213> E. Coli

<400> 344
Met Arg Ala Arg Glu Gln Val Ala Lys Ile Val Ser Lys Asn Asp Pro
1 5 10 15
Asp Thr Lys Lys Val Trp Cys Lys Tyr Gly Lys Ile Pro Gly Gln Gly
20 25 30
Asp Gly Val Asn Leu Phe Phe Val Gly Glu Ile Asn Val Thr His Tyr
35 40 45
Phe Ile Thr Asn Ile Gly Ala Gly Leu Pro Asp Ala Cys Ala Glu
50 55 60

<210> 345
<211> 167
<212> PRT
<213> E. Coli

<400> 345
Met Pro Gly Asn Ser Pro His Tyr Gly Arg Trp Pro Gln His Asp Phe
1 5 10 15
Thr Ser Leu Lys Lys Leu Arg Pro Gln Ser Val Thr Ser Arg Ile Gln
20 25 30
Pro Gly Ser Asp Val Ile Val Cys Ala Glu Met Asp Glu Gln Trp Gly
35 40 45
Tyr Val Gly Ala Lys Ser Arg Gln Arg Trp Leu Phe Tyr Ala Tyr Asp
50 55 60
Ser Leu Arg Lys Thr Val Val Ala His Val Phe Gly Glu Arg Thr Met
65 70 75 80
Ala Thr Leu Gly Arg Leu Met Ser Leu Leu Ser Pro Phe Asp Val Val
85 90 95
Ile Trp Met Thr Asp Gly Trp Pro Leu Tyr Glu Ser Arg Leu Lys Gly
100 105 110
Lys Leu His Val Ile Ser Lys Arg Tyr Thr Gln Arg Ile Glu Arg His
115 120 125
Asn Leu Asn Leu Arg Gln His Leu Ala Arg Leu Gly Arg Lys Ser Leu
130 135 140
Ser Phe Ser Lys Ser Val Glu Leu His Asp Lys Val Ile Gly His Tyr
145 150 155 160
Leu Asn Ile Lys His Tyr Gln
165

<210> 346
<211> 91
<212> PRT
<213> E. Coli

<400> 346
Met Ala Ser Val Ser Ile Ser Cys Pro Ser Cys Ser Ala Thr Asp Gly
1 5 10 15
Val Val Arg Asn Gly Lys Ser Thr Ala Gly His Gln Arg Tyr Leu Cys
20 25 30
Ser His Cys Arg Lys Thr Trp Gln Leu Gln Phe Thr Tyr Thr Ala Ser
35 40 45
Gln Pro Gly Thr His Gln Lys Ile Ile Asp Met Ala Met Asn Gly Val
50 55 60
Gly Cys Arg Ala Thr Ala Arg Ile Met Gly Val Gly Leu Asn Thr Ile
65 70 75 80
Leu Arg His Leu Lys Asn Ser Gly Arg Ser Arg
85 90

<210> 347
<211> 158
<212> PRT
<213> E. Coli

<400> 347
Met Met Thr Lys Thr Gln Ile Asn Lys Leu Ile Lys Met Met Asn Asp
1 5 10 15
Leu Asp Tyr Pro Phe Glu Ala Pro Leu Lys Glu Ser Phe Ile Glu Ser
20 25 30
Ile Ile Gln Ile Glu Phe Asn Ser Asn Ser Thr Asn Cys Leu Glu Lys
35 40 45
Leu Cys Asn Glu Val Ser Ile Leu Phe Lys Asn Gln Pro Asp Tyr Leu
50 55 60
Thr Phe Leu Arg Ala Met Asp Gly Phe Glu Val Asn Gly Leu Arg Leu
65 70 75 80
Phe Ser Leu Ser Ile Pro Glu Pro Ser Val Lys Asn Leu Phe Ala Val
85 90 95
Asn Gln Phe Tyr Arg Asn Asn Asp Asp Phe Ile Asn Pro Asp Leu Gln
100 105 110
Glu Arg Leu Val Ile Gly Asp Tyr Ser Ile Ser Ile Phe Thr Tyr Asp
115 120 125
Ile Lys Gly Asp Ala Ala Asn Leu Leu Ile
130 135

<210> 348
<211> 342
<212> PRT
<213> E. Coli

<400> 348
Met Ser Asn Ile Val Tyr Leu Thr Val Thr Gly Glu Gln Gln Gly Ser
1 5 10 15
Ile Ser Ala Gly Cys Gly Thr Ser Glu Ser Thr Gly Asn Arg Trp Gln

```
                20                  25                  30
Ser Gly His Glu Asp Glu Ile Phe Thr Phe Ser Leu Leu Asn Asn Ile
            35                  40                  45
Asn Asn Thr Gly Leu Gly Ser Gln Phe His Gly Ile Thr Phe Cys Lys
        50                  55                  60
Leu Ile Asp Lys Ser Thr Pro Leu Phe Ile Asn Ser Ile Asn Asn Asn
    65                  70                  75                  80
Glu Gln Leu Phe Met Gly Phe Asp Phe Tyr Arg Ile Asn Arg Phe Gly
                85                  90                  95
Arg Leu Glu Lys Tyr Tyr Tyr Ile Gln Leu Arg Gly Ala Phe Leu Ser
            100                 105                 110
Ala Ile His His Gln Ile Ile Glu Asn Gln Leu Asp Thr Glu Thr Ile
        115                 120                 125
Thr Ile Ser Tyr Glu Phe Ile Leu Lys Gln His Leu Ile Ala Asn Thr
    130                 135                 140
Glu Phe Ser Tyr Leu Ala Leu Pro Glu Asn Tyr Asn Arg Leu Phe Leu
145                 150                 155                 160
Pro Asn Ser Lys Asn Gln Thr Asn Asn Arg Phe Lys Thr Leu Asn Ser
                165                 170                 175
Lys Ala Ile Gly Arg Leu Leu Ala Ala Gly Gly Val Tyr Asn Gly Asn
            180                 185                 190
Ile Glu Gly Phe Arg Asp Thr Ala Glu Lys Leu Gly Gly Asp Ala Ile
        195                 200                 205
Lys Gly Tyr Asp Gln Ile Leu Asn Glu Lys Thr Ala Gly Ile Ala Ile
    210                 215                 220
Ala Thr Ala Leu Ile Leu Leu Thr Lys Arg Ser Asn Val Asp Thr Tyr
225                 230                 235                 240
Thr Glu Ile Asn Ser Tyr Leu Gly Lys Leu Arg Gly Gln Gln Lys Leu
                245                 250                 255
Leu Asp Gly Ile Asp Ile Ile Glu Ile Ile Tyr Ile Lys Arg Pro Ser
            260                 265                 270
Lys Asp Leu Ala Asn Leu Arg Lys Glu Phe Asn Lys Thr Val Arg Lys
        275                 280                 285
Asn Phe Leu Ile Lys Leu Ala Lys Thr Ser Glu Ala Ser Gly Arg Phe
    290                 295                 300
Asn Ala Glu Asp Leu Leu Arg Met Arg Lys Gly Asn Val Pro Leu Asn
305                 310                 315                 320
Tyr Asn Val His His Lys Leu Ser Leu Asp Asp Gly Gly Thr Asn Asp
                325                 330                 335
Phe Gln Asn Leu Val Leu Ile Glu Asn Glu Pro Tyr His Lys Val Phe
            340                 345                 350
Thr Asn Met Gln Ser Arg Ile Ala Lys Gly Ile Leu Val Gly Glu Ser
        355                 360                 365
Lys Ile Thr Pro Trp Ala Ile Pro Ser Gly Ser Ile Tyr Pro Pro Met
    370                 375                 380
Lys Asn Ile Met Asp His Thr Lys
385                 390
```

<210> 849
<211> 771
<212> PRT
<213> E. Coli

<400> 849

```
Met Val Leu Ala Leu Asn Tyr Asn Met His Gly Val Asn Ile Arg Ser
```

```
 1               5                  10                  15
Glu Asn Ala Ala Lys Pro His Thr Met Pro Ser Arg Tyr Leu Cys Glu
            20                  25                  30
Tyr Ile Arg Ser Ile Glu Lys Asn Gly His Ala Leu Asp Phe Gly Cys
        35                  40                  45
Gly Lys Leu Arg Tyr Ser Asp Glu Leu Ile Ser Lys Phe Asp Glu Val
    50                  55                  60
Thr Phe Leu Asp Ser Lys Arg Gln Leu Glu Arg Glu Gln Ile Ile Arg
65                  70                  75                  80
Gly Ile Lys Thr Lys Ile Ile Asp Tyr Val Pro Arg Tyr Tyr Lys Asn
                85                  90                  95
Ala Asn Thr Val Ala Phe Glu Asp Val Asp Lys Ile Ile Gly Gly Tyr
            100                 105                 110
Asp Phe Ile Leu Cys Ser Asn Val Leu Ser Ala Val Pro Asp Arg Asp
        115                 120                 125
Thr Ile Asp Lys Ile Val Leu Ser Ile Lys Arg Leu Leu Lys Ser Gly
    130                 135                 140
Gly Glu Thr Leu Ile Val Asn Gln Tyr Lys Ser Ser Tyr Phe Lys Lys
145                 150                 155                 160
Tyr Glu Thr Gly Arg Lys His Leu Tyr Gly Tyr Ile Tyr Lys Asn Ser
                165                 170                 175
Lys Ser Val Ser Tyr Tyr Gly Leu Leu Asp Glu Leu Ala Val Gln Glu
            180                 185                 190
Ile Cys Ser Ser His Gly Leu Glu Ile Leu Lys Ser Trp Ser Lys Ala
        195                 200                 205
Gly Ser Ser Tyr Val Thr Val Gly Ser Cys Asn Ala Ile
    210                 215                 220
```


(210) 61
(211) 234
(212) PRT
(213) E. Coli

(400) 61


```
Met Asn Asn Met Phe Glu Pro Pro Lys Asn Tyr Asn Glu Met Leu Pro
 1               5                  10                  15
Lys Leu His Lys Ala Thr Phe Leu Asn Thr Leu Ile Tyr Cys Ile Leu
            20                  25                  30
Leu Val Ile Tyr Glu Tyr Ile Pro Leu Ile Thr Leu Pro Thr Lys Tyr
        35                  40                  45
Val Pro Pro Ile Lys Asp His Glu Ser Phe Ile Asn Trp Ala Leu Ser
    50                  55                  60
Phe Gly Ile Leu Pro Cys Ala Phe Ala Ile Phe Ala Tyr Leu Ile Ser
65                  70                  75                  80
Gly Ala Leu Asp Leu His Asn Asn Ala Ala Lys Leu Leu Arg Val Arg
                85                  90                  95
Tyr Leu Trp Asp Lys His Leu Ile Ile Lys Pro Leu Ser Arg Arg Ala
            100                 105                 110
Gly Val Asn Arg Lys Leu Asn Lys Asp Glu Ala His Asn Val Met Ser
        115                 120                 125
Asn Leu Tyr Tyr Pro Glu Val Arg Lys Ile Glu Asp Lys His Tyr Ile
    130                 135                 140
Glu Leu Phe Trp Asn Lys Val Tyr Tyr Phe Trp Ile Phe Phe Glu Phe
145                 150                 155                 160
Ser Ile Ile Ala Leu Ile Ser Phe Leu Ile Ile Phe Phe Cys Lys Gln
                165                 170                 175
```

Met Asp Ile Phe His Val Glu Gly Ser Leu Leu Ser Leu Phe Phe Phe
180 185 190
Val Ile Leu Ser Phe Ser Val Ser Gly Ile Ile Phe Ala Leu Thr Val
195 200 205
Lys Pro Arg Thr Glu Ser Gln Val Gly Lys Ile Pro Asp Asp Lys Ile
210 215 220
Lys Glu Phe Phe Thr Lys Asn Asn Ile Asn
225 230

<210> 351
<211> 44
<212> PRT
<213> E. Coli

<400> 351
Met Phe Thr Ile Asn Ala Glu Val Arg Lys Glu Gln Gly Lys Gly Ala
1 5 10 15
Ser Arg Arg Leu Arg Ala Ala Asn Lys Phe Pro Ala Ile Ile Tyr Gly
20 25 30
Gly Lys Glu Ala Pro Leu Ala Ile Glu Leu Asp His Asp Lys Val Met
35 40 45
Asn Met Gln Ala Lys Ala Glu Phe Tyr Ser Glu Val Leu Thr Ile Val
50 55 60
Val Asp Gly Lys Glu Ile Lys Val Lys Ala Gln Asp Val Gln Arg His
65 70 75 80
Pro Tyr Lys Pro Lys Leu Gln His Ile Asp Phe Val Arg Ala
85 90

<210> 352
<211> 458
<212> PRT
<213> E. Coli

<400> 352
Met Val Leu Phe Tyr Arg Ala His Trp Arg Asp Tyr Lys Asn Asp Gln
1 5 10 15
Val Arg Ile Met Met Asn Leu Thr Thr Leu Thr His Arg Asp Ala Leu
20 25 30
Cys Leu Asn Ala Arg Phe Thr Ser Arg Glu Glu Ala Ile His Ala Leu
35 40 45
Thr Gln Arg Leu Ala Ala Leu Gly Lys Ile Ser Ser Thr Glu Gln Phe
50 55 60
Leu Glu Glu Val Tyr Arg Arg Glu Ser Leu Gly Pro Thr Ala Leu Gly
65 70 75 80
Glu Gly Leu Ala Val Pro His Gly Lys Thr Ala Ala Val Lys Glu Ala
85 90 95
Ala Phe Ala Val Ala Thr Leu Ser Glu Pro Leu Gln Trp Glu Gly Val
100 105 110
Asp Gly Pro Glu Ala Val Asp Leu Val Val Leu Leu Ala Ile Pro Pro
115 120 125
Asn Glu Ala Gly Thr Thr His Met Gln Leu Leu Thr Ala Leu Thr Thr
130 135 140
Arg Leu Ala Asp Asp Glu Ile Arg Ala Arg Ile Gln Ser Ala Thr Thr
145 150 155 160

Pro Asp Glu Leu Leu Ser Ala Leu Asp Asp Lys Gly Gly Thr Gln Pro
165 170 175
Ser Ala Ser Phe Ser Asn Ala Pro Thr Ile Val Cys Val Thr Ala Cys
180 185 190
Pro Ala Gly Ile Ala His Thr Tyr Met Ala Ala Glu Tyr Leu Glu Lys
195 200 205
Ala Gly Arg Lys Leu Gly Val Asn Val Tyr Val Glu Lys Gln Gly Ala
210 215 220
Asn Gly Ile Glu Gly Arg Leu Thr Ala Asp Gln Leu Asn Ser Ala Thr
225 230 235 240
Ala Cys Ile Pro Ala Ala Glu Val Ala Ile Lys Glu Ser Glu Arg Phe
245 250 255
Asn Gly Ile Pro Ala Leu Ser Val Pro Val Ala Leu Pro Ile Arg His
260 265 270
Ala Gln Ala Leu Ile Gln Gln Ala Leu Thr Leu Lys Arg Ser Asp Glu
275 280 285
Thr Arg Thr Val Gln Gln Asp Thr Gln Pro Val Lys Ser Val Lys Thr
290 295 300
Glu Leu Lys Gln Ala Leu Leu Ser Gly Ile Ser Phe Ala Val Pro Leu
305 310 315 320
Ile Val Ala Gly Gly Thr Val Leu Ala Val Ala Val Leu Leu Ser Gln
325 330 335
Ile Phe Gly Leu Gln Asp Leu Phe Asn Glu Glu Asn Ser Trp Leu Trp
340 345 350
Met Tyr Arg Lys Leu Gly Gly Gly Leu Leu Gly Ile Leu Met Val Pro
355 360 365
Val Leu Ala Ala Tyr Thr Ala Tyr Ser Leu Ala Asp Lys Pro Ala Leu
370 375 380
Ala Pro Gly Phe Ala Ala Gly Leu Ala Ala Asn Met Ile Gly Ser Gly
385 390 395 400
Phe Leu Gly Ala Val Val Gly Gly Leu Ile Ala Gly Tyr Leu Met Arg
405 410 415
Trp Val Lys Asn His Leu Arg Leu Ser Ser Lys Phe Asn Gly Phe Leu
420 425 430
Thr Phe Tyr Leu Tyr Pro Val Leu Gly Thr Leu Gly Ala Gly Ser Leu
435 440 445
Met Leu Phe Val Val Gly Glu Pro Val Ala Trp Ile Asn Asn Ser Leu
450 455 460
Thr Ala Trp Leu Asn Gly Leu Ser Gly Ser Asn Ala Leu Leu Leu Gly
465 470 475 480
Ala Ile Leu Gly Phe Met Tyr Ser Phe Asp Leu Gly Gly Pro Val Asn
485 490 495
Lys Ala Ala Tyr Ala Phe Cys Leu Gly Ala Met Ala Asn Gly Val Tyr
500 505 510
Gly Pro Tyr Ala Ile Phe Ala Ser Val Lys Met Val Ser Ala Phe Thr
515 520 525
Val Thr Ala Ser Thr Met Leu Ala Pro Arg Leu Phe Lys Glu Phe Gln
530 535 540
Ile Gln Thr Gly Lys Ser Thr Trp Leu Leu Gly Leu Ala Gly Ile Thr
545 550 555 560
Glu Gly Ala Ile Pro Met Ala Leu Glu Asp Pro Leu Arg Val Ile Gly
565 570 575
Ser Phe Val Leu Gly Ser Met Val Thr Gly Ala Ile Val Gly Ala Met
580 585 590
Asn Ile Gly Leu Ser Thr Pro Gly Ala Gly Ile Phe Ser Leu Phe Leu
595 600 605
Leu His Asp Asn Gly Ala Gly Gly Val Met Ala Ala Ile Gly Trp Phe

610 615 620

Gly Ala Ala Leu Val Gly Ala Ala Ile Ser Thr Ala Ile Leu Leu Met
625 630 635 640

Trp Arg Arg His Ala Val Lys His Gly Asn Tyr Leu Thr Asp Gly Val
645 650 655

Met Pro

<210> 363
<211> 377
<212> PRT
<213> E. Coli

<400> 363

Met Lys Ala Val Ser Arg Val His Ile Thr Pro His Met His Trp Asp
1 5 10 15

Arg Glu Trp Tyr Phe Thr Thr Glu Glu Ser Arg Ile Leu Leu Val Asn
20 25 30

Asn Met Glu Glu Ile Leu Cys Arg Leu His Gln Asp Asn Glu Tyr Lys
35 40 45

Tyr Tyr Val Leu Asp Gly Gln Thr Ala Ile Leu Glu Asp Tyr Phe Ala
50 55 60

Val Lys Pro Glu Asn Lys Asp Arg Val Lys Lys Gln Val Glu Ala Gly
65 70 75 80

Lys Leu Ile Ile Gly Pro Trp Tyr Thr Gln Thr Asp Thr Thr Ile Val
85 90 95

Ser Ala Glu Ser Ile Val Arg Asn Leu Met Tyr Gly Met Arg Asp Cys
100 105 110

Leu Ala Phe Gly Glu Pro Met Lys Ile Gly Tyr Leu Pro Asp Ser Phe
115 120 125

Gly Met Ser Gly Gln Leu Pro His Ile Tyr Asn Gly Phe Gly Ile Thr
130 135 140

Arg Thr Met Phe Trp Arg Gly Val Ser Gln Arg His Gly Thr Asp Lys
145 150 155 160

Thr Glu Phe Leu Trp Gln Ser Ser Asp Gly Ser Glu Val Thr Ala Gln
165 170 175

Val Leu Pro Leu Gly Tyr Ala Ile Gly Lys Tyr Leu Pro Ala Asp Glu
180 185 190

Asn Gly Leu Arg Lys Arg Leu Asp Ser Tyr Phe Asp Val Leu Glu Lys
195 200 205

Ala Ser Val Thr Lys Glu Ile Leu Leu Pro Asn Gly His Asp Gln Met
210 215 220

Pro Leu Gln Gln Asn Ile Phe Glu Val Met Asp Lys Leu Arg Glu Ile
225 230 235 240

Tyr Pro Gln Arg Lys Phe Val Met Ser Arg Phe Glu Glu Val Phe Glu
245 250 255

Lys Ile Gln Ala Gln Arg Asp Asn Leu Ala Thr Leu Lys Gly Glu Phe
260 265 270

Ile Asp Gly Lys Tyr Met Arg Val His Arg Thr Ile Gly Ser Thr Arg
275 280 285

Met Asp Ile Lys Ile Ala His Ala Arg Ile Glu Asn Lys Ile Val Asn
290 295 300

Leu Leu Glu Pro Leu Ala Thr Leu Ala Trp Thr Leu Gly Phe Glu Tyr
305 310 315 320

His His Gly Leu Leu Glu Lys Met Trp Lys Glu Ile Leu Lys Asn His
325 330 335

Ala His Asp Ser Ile Gly Cys Cys Cys Ser Asp Lys Val His Arg Glu
340 345 350
Ile Val Ala Arg Phe Glu Leu Ala Glu Asp Met Ala Asp Asn Leu Ile
355 360 365
Arg Phe Tyr Met Arg Lys Ile Ala Asp Asn Met Pro Gln Ser Asp Ala
370 375 380
Asp Lys Leu Val Leu Phe Asn Leu Met Pro Trp Pro Arg Glu Glu Val
385 390 395 400
Ile Asn Thr Thr Val Arg Leu Arg Ala Ser Gln Phe Asn Leu Arg Asp
405 410 415
Asp Arg Gly Gln Pro Val Pro Tyr Phe Ile Arg His Ala Arg Glu Ile
420 425 430
Asp Pro Gly Leu Ile Asp Arg Gln Ile Val His Tyr Gly Asn Tyr Asp
435 440 445
Pro Phe Met Glu Phe Asp Ile Gln Ile Asn Gln Ile Val Pro Ser Met
450 455 460
Gly Tyr Arg Thr Leu Tyr Ile Glu Ala Asn Gln Pro Gly Asn Val Ile
465 470 475 480
Ala Ala Lys Ser Asp Ala Glu Gly Ile Leu Glu Asn Ala Phe Trp Gln
485 490 495
Ile Ala Leu Asn Glu Asp Gly Ser Leu Gln Leu Val Asp Lys Asp Ser
500 505 510
Gly Val Arg Tyr Asp Arg Val Leu Gln Ile Glu Glu Ser Ser Asp Asp
515 520 525
Gly Asp Glu Tyr Asp Tyr Ser Pro Ala Lys Glu Glu Trp Val Ile Thr
530 535 540
Ala Ala Asn Ala Lys Pro Gln Cys Asp Ile Ile His Glu Ala Trp Gln
545 550 555 560
Ser Arg Ala Val Ile Arg Tyr Asp Met Ala Val Pro Leu Asn Leu Ser
565 570 575
Glu Arg Ser Ala Arg Gln Ser Thr Gly Arg Val Gly Val Val Leu Val
580 585 590
Val Thr Leu Ser His Asn Ser Arg Arg Ile Asp Val Asp Ile Asn Leu
595 600 605
Asp Asn Gln Ala Asp Asp His Arg Leu Arg Val Leu Val Pro Thr Pro
610 615 620
Phe Asn Thr Asp Ser Val Leu Ala Asp Thr Gln Phe Gly Ser Leu Thr
625 630 635 640
Arg Pro Val Asn Asp Ser Ala Met Asn Asn Trp Gln Gln Glu Gly Trp
645 650 655
Lys Gln Ala Pro Val Pro Val Trp Asn Met Leu Asn Tyr Val Ala Leu
660 665 670
Gln Gln Gly Arg Asn Gly Met Ala Val Phe Ser Glu Gly Leu Arg Glu
675 680 685
Phe Glu Val Ile Gly Glu Glu Lys Lys Thr Phe Ala Ile Thr Leu Leu
690 695 700
Arg Gly Val Gly Leu Leu Gly Lys Glu Asp Leu Leu Leu Arg Pro Gly
705 710 715 720
Arg Pro Ser Gly Ile Lys Met Pro Val Pro Asp Ser Gln Leu Arg Gly
725 730 735
Leu Leu Ser Cys Arg Leu Ser Leu Leu Ser Tyr Thr Gly Thr Pro Thr
740 745 750
Ala Ala Gly Val Ala Gln Gln Ala Arg Ala Trp Leu Thr Pro Val Gln
755 760 765
Cys Tyr Asn Lys Ile Pro Trp Asp Val Met Lys Leu Asn Lys Ala Gly
770 775 780
Phe Asn Val Pro Glu Ser Tyr Ser Leu Leu Lys Met Pro Pro Val Gly

785 790 795 800

Cys Leu Ile Ser Ala Leu Lys Lys Ala Glu Asp Arg Gln Glu Val Ile
805 810 815

Leu Arg Leu Phe Asn Pro Ala Glu Ser Ala Thr Cys Asp Ala Thr Val
820 825 830

Ala Phe Ser Arg Glu Val Ile Ser Cys Ser Glu Thr Met Met Asp Glu
835 840 845

His Ile Thr Thr Glu Glu Asn Gln Gly Ser Asn Leu Ser Gly Pro Phe
850 855 860

Leu Pro Gly Gln Ser Arg Thr Phe Ser Tyr Arg Leu Ala
865 870 875

<210> 364
<211> 878
<212> PRT
<213> E. Coli

<400> 364

Met Met Leu Asp Ile Val Glu Leu Ser Arg Leu Gln Phe Ala Leu Thr
1 5 10 15

Ala Met Tyr His Phe Leu Phe Val Pro Leu Thr Leu Gly Met Ala Phe
20 25 30

Leu Leu Ala Ile Met Glu Thr Val Tyr Val Leu Ser Gly Lys Gln Ile
35 40 45

Tyr Lys Asp Met Thr Lys Phe Trp Gly Lys Leu Phe Gly Ile Asn Phe
50 55 60

Ala Leu Gly Val Ala Thr Gly Leu Thr Met Glu Phe Gln Phe Gly Thr
65 70 75 80

Asn Trp Ser Tyr Tyr Ser His Tyr Val Gly Asp Ile Phe Gly Ala Pro
85 90 95

Leu Ala Ile Glu Gly Leu Met Ala Phe Phe Leu Glu Ser Thr Phe Val
100 105 110

Gly Leu Phe Phe Phe Gly Trp Asp Arg Leu Gly Lys Val Gln His Met
115 120 125

Cys Val Thr Trp Leu Val Ala Leu Gly Ser Asn Leu Ser Ala Leu Trp
130 135 140

Ile Leu Val Ala Asn Gly Trp Met Gln Asn Pro Ile Ala Ser Asp Phe
145 150 155 160

Asn Phe Glu Thr Met Arg Met Glu Met Val Ser Phe Ser Glu Leu Val
165 170 175

Leu Asn Pro Val Ala Gln Val Lys Phe Val His Thr Val Ala Ser Gly
180 185 190

Tyr Val Thr Gly Ala Met Phe Ile Leu Gly Ile Ser Ala Trp Tyr Met
195 200 205

Leu Lys Gly Arg Asp Phe Ala Phe Ala Lys Arg Ser Phe Ala Ile Ala
210 215 220

Ala Ser Phe Gly Met Ala Ala Val Leu Ser Val Ile Val Leu Gly Asp
225 230 235 240

Glu Ser Gly Tyr Glu Met Gly Asp Val Gln Lys Thr Lys Leu Ala Ala
245 250 255

Ile Glu Ala Glu Trp Glu Thr Gln Pro Ala Pro Ala Ala Phe Thr Leu
260 265 270

Phe Gly Ile Pro Asp Gln Glu Glu Glu Thr Asn Lys Phe Ala Ile Gln
275 280 285

Ile Pro Tyr Ala Leu Gly Ile Ile Ala Thr Arg Ser Val Asp Thr Pro
290 295 300

Val Ile Gly Leu Lys Glu Leu Met Val Gln His Glu Glu Arg Ile Arg
305 310 315 320
Asn Gly Met Lys Ala Tyr Ser Leu Leu Glu Gln Leu Arg Ser Gly Ser
325 330 335
Thr Asp Gln Ala Val Arg Asp Gln Phe Asn Ser Met Lys Lys Asp Leu
340 345 350
Gly Tyr Gly Leu Leu Leu Leu Lys Arg Tyr Thr Pro Asn Val Ala Asp Ala
355 360 365
Thr Glu Ala Gln Ile Gln Gln Ala Thr Lys Asp Ser Ile Pro Arg Val
370 375 380
Ala Pro Leu Tyr Phe Ala Phe Arg Ile Met Val Ala Cys Gly Phe Leu
385 390 395 400
Leu Leu Ala Ile Ile Ala Leu Ser Phe Trp Ser Val Ile Arg Asn Arg
405 410 415
Ile Gly Gln Lys Lys Trp Leu Leu Arg Ala Ala Leu Tyr Gly Ile Pro
420 425 430
Leu Pro Trp Ile Ala Val Glu Ala Gly Trp Phe Val Ala Gln Tyr Gly
435 440 445
Arg Gln Pro Trp Ala Ile Gly Glu Val Leu Pro Thr Ala Val Ala Asn
450 455 460
Ser Ser Leu Thr Ala Gly Asp Leu Ile Phe Ser Met Val Leu Ile Cys
465 470 475 480
Gly Leu Tyr Thr Leu Phe Leu Val Ala Glu Leu Phe Leu Met Phe Lys
485 490 495
Phe Ala Arg Leu Gly Pro Ser Ser Leu Lys Thr Gly Arg Tyr His Phe
500 505 510
Gln Gln Ser Ser Thr Thr Thr Gln Pro Ala Arg
515 520

<210> 335
<211> 379
<212> PRT
<213> E. Coli

<400> 335
Met Ile Asp Tyr Glu Val Leu Arg Phe Ile Trp Trp Leu Leu Val Gly
1 5 10 15
Val Leu Leu Ile Gly Phe Ala Val Thr Asp Gly Phe Asp Met Gly Val
20 25 30
Gly Met Leu Thr Arg Phe Leu Gly Arg Asn Asp Thr Glu Arg Arg Ile
35 40 45
Met Ile Asn Ser Ile Ala Pro His Trp Asp Gly Asn Gln Val Trp Leu
50 55 60
Ile Thr Ala Gly Gly Ala Leu Phe Ala Ala Trp Pro Met Val Tyr Ala
65 70 75 80
Ala Ala Phe Ser Gly Phe Tyr Val Ala Met Ile Leu Val Leu Ala Ser
85 90 95
Leu Phe Phe Arg Pro Val Gly Phe Asp Tyr Arg Ser Lys Ile Glu Glu
100 105 110
Thr Arg Trp Arg Asn Met Trp Asp Trp Gly Ile Phe Ile Gly Ser Phe
115 120 125
Val Pro Pro Leu Val Ile Gly Val Ala Phe Gly Asn Leu Leu Gln Gly
130 135 140
Val Pro Phe Asn Val Asp Glu Tyr Leu Arg Leu Tyr Tyr Thr Gly Asn
145 150 155 160
Phe Phe Gln Leu Leu Asn Pro Phe Gly Leu Leu Ala Gly Val Val Ser

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                165                     170                     175
Val Gly Met Ile Ile Thr Gln Gly Ala Thr Tyr Leu Gln Met Arg Thr
            180                     185                     190
Val Gly Glu Leu His Leu Arg Thr Arg Ala Thr Ala Gln Val Ala Ala
        195                     200                     205
Leu Val Thr Leu Val Cys Phe Ala Leu Ala Gly Val Trp Val Met Tyr
    210                     215                     220
Gly Ile Asp Gly Tyr Val Val Lys Ser Thr Met Asp His Tyr Ala Ala
225                     230                     235                     240
Ser Asn Pro Leu Asn Lys Glu Val Val Arg Glu Ala Gly Ala Trp Leu
                245                     250                     255
Val Asn Phe Asn Asn Thr Pro Ile Leu Trp Ala Ile Pro Ala Leu Gly
            260                     265                     270
Val Val Leu Pro Leu Leu Thr Ile Leu Thr Ala Arg Met Asp Lys Ala
        275                     280                     285
Ala Trp Ala Phe Val Phe Ser Ser Leu Thr Leu Ala Cys Ile Ile Leu
    290                     295                     300
Thr Ala Gly Ile Ala Met Phe Pro Phe Val Met Pro Ser Ser Thr Met
305                     310                     315                     320
Met Asn Ala Ser Leu Thr Met Trp Asp Ala Thr Ser Ser Gln Leu Thr
                325                     330                     335
Leu Asn Val Met Thr Trp Val Ala Val Val Leu Val Pro Ile Ile Leu
            340                     345                     350
Leu Tyr Thr Ala Trp Cys Tyr Trp Lys Met Phe Gly Arg Ile Thr Lys
        355                     360                     365
Glu Asp Ile Glu Arg Asn Thr His Ser Leu Tyr
    370                     375
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<210> 356
<211> 456
<212> PRT
<213> E. Coli

<400> 356

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Met Glu Leu Ser Ser Leu Thr Ala Val Ser Pro Val Asp Gly Arg Tyr
 1               5                  10                  15
Gly Asp Lys Val Ser Ala Leu Arg Gly Ile Phe Ser Glu Tyr Gly Leu
            20                  25                  30
Leu Lys Phe Arg Val Gln Val Glu Val Arg Trp Leu Gln Lys Leu Ala
        35                  40                  45
Ala His Ala Ala Ile Lys Glu Val Pro Ala Phe Ala Ala Asp Ala Ile
    50                  55                  60
Gly Tyr Leu Asp Ala Ile Val Ala Ser Phe Ser Glu Glu Asp Ala Ala
65                  70                  75                  80
Arg Ile Lys Thr Ile Glu Arg Thr Thr Asn His Asp Val Lys Ala Val
                85                  90                  95
Glu Tyr Phe Leu Lys Glu Lys Val Ala Glu Ile Pro Glu Leu His Ala
            100                 105                 110
Val Ser Glu Phe Ile His Phe Ala Cys Thr Ser Glu Asp Ile Asn Asn
        115                 120                 125
Leu Ser His Ala Leu Met Leu Lys Thr Ala Arg Asp Glu Val Ile Leu
    130                 135                 140
Pro Tyr Trp Arg Gln Leu Ile Asp Gly Ile Lys Asp Leu Ala Val Gln
145                 150                 155                 160
Tyr Arg Asp Ile Pro Leu Leu Ser Arg Thr His Gly Gln Pro Ala Thr
                165                 170                 175
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Pro Ser Thr Ile Gly Lys Glu Met Ala Asn Val Ala Tyr Arg Met Glu
160 165 190
Arg Gln Tyr Arg Gln Leu Asn Gln Val Glu Ile Leu Gly Lys Ile Asn
170 180 200
Gly Ala Val Gly Asn Tyr Asn Ala His Ile Ala Ala Tyr Pro Glu Val
210 215 220
Asp Trp His Gln Phe Ser Glu Glu Phe Val Thr Ser Leu Gly Ile Gln
225 230 235 240
Trp Asn Pro Tyr Thr Thr Gln Ile Glu Pro His Asp Tyr Ile Ala Glu
245 250 255
Leu Phe Asp Cys Val Ala Arg Phe Asn Thr Ile Leu Ile Asp Phe Asp
260 265 270
Arg Asp Val Trp Gly Tyr Ile Ala Leu Asn His Phe Lys Gln Lys Thr
275 280 285
Ile Ala Gly Glu Ile Gly Ser Ser Thr Met Pro His Lys Val Asn Pro
290 295 300
Ile Asp Phe Glu Asn Ser Glu Gly Asn Leu Gly Leu Ser Asn Ala Val
305 310 315 320
Leu Gln His Leu Ala Ser Lys Leu Pro Val Ser Arg Trp Gln Arg Asp
325 330 335
Leu Thr Asp Ser Thr Val Leu Arg Asn Leu Gly Val Gly Ile Gly Tyr
340 345 350
Ala Leu Ile Ala Tyr Gln Ser Thr Leu Lys Gly Val Ser Lys Leu Glu
355 360 365
Val Asn Asn Asp His Leu Leu Asp Glu Leu Asp His Asn Trp Glu Val
370 375 380
Leu Ala Glu Pro Ile Gln Thr Val Met Arg Arg Tyr Gly Ile Glu Lys
385 390 395 400
Pro Tyr Glu Lys Leu Lys Glu Leu Thr Arg Gly Lys Arg Val Asp Ala
405 410 415
Glu Gly Met Lys Gln Phe Ile Asp Gly Leu Ala Leu Pro Glu Glu Glu
420 425 430
Lys Ala Asn Leu Lys Ala Met Thr Pro Ala Asn Tyr Ile Gly Arg Ala
435 440 445
Ile Thr Met Val Asp Glu Leu Lys
450 455

<210> 347
<211> 61
<212> PRT
<213> E. Coli

<400> 347
Met Leu Ile Leu Thr Arg Arg Val Gly Glu Thr Leu Met Ile Gly Asp
1 5 10 15
Glu Val Thr Val Thr Val Leu Gly Val Lys Gly Asn Gln Val Arg Ile
20 25 30
Gly Val Asn Ala Pro Lys Glu Val Ser Val His Arg Glu Glu Ile Tyr
35 40 45
Gln Arg Ile Gln Ala Glu Lys Ser Gln Gln Ser Ser Tyr
50 55 60

<210> 348
<211> 83
<212> RNA

<213> E. Coli

<400> 358

ggugaggugg ccuagaggcu gaaggcgcuc ccugcuaaag ggaguaugcg gucaaaagcu 60
gcaucccggg uucgaauccc cgccucaccg cca 83

<210> 359
<211> 240
<212> PRT
<213> E. Coli

<400> 359

Met Lys Asn Lys Ala Asp Asn Lys Lys Arg Asn Phe Leu Thr His Ser
1 5 10 15
Glu Ile Gln Ser Leu Leu Lys Ala Ala Asn Thr Gly Pro His Ala Ala
20 25 30
Arg Asn Tyr Cys Leu Thr Leu Leu Cys Phe Ile His Gly Phe Arg Ala
35 40 45
Ser Gln Ile Cys Arg Leu Arg Ile Ser Asp Ile Asp Leu Lys Ala Lys
50 55 60
Cys Ile Tyr Ile His Arg Leu Lys Lys Gly Phe Ser Thr Thr His Pro
65 70 75 80
Leu Leu Asn Lys Glu Val Gln Ala Leu Lys Asn Trp Leu Ser Ile Arg
85 90 95
Thr Ser Tyr Pro His Ala Glu Ser Glu Trp Val Phe Leu Ser Arg Lys
100 105 110
Gly Asn Pro Leu Ser Arg Gln Gln Phe Tyr His Ile Ile Ser Thr Ser
115 120 125
Gly Gly Asn Ala Gly Leu Ser Leu Glu Ile His Pro His Met Leu Arg
130 135 140
His Ser Cys Gly Phe Ala Leu Ala Asn Met Gly Ile Asp Thr Arg Leu
145 150 155 160
Ile Gln Asp Tyr Leu Gly His Arg Asn Ile Arg His Thr Val Trp Tyr
165 170 175
Thr Ala Ser Asn Ala Gly Arg Phe Tyr Gly Ile Trp Asp Arg Ala Arg
180 185 190
Gly Arg Gln Arg His Ala Val Leu
195 200

<210> 360
<211> 145
<212> PRT
<213> E. Coli

<400> 360

Met Ser Lys Arg Arg Tyr Leu Thr Gly Lys Glu Val Gln Ala Met Met
1 5 10 15
Gln Ala Val Cys Tyr Gly Ala Thr Gly Ala Arg Asp Tyr Cys Leu Ile
20 25 30
Leu Leu Ala Tyr Arg His Gly Met Arg Ile Ser Glu Leu Leu Asp Leu
35 40 45
His Tyr Gln Asp Leu Asp Leu Asn Glu Gly Arg Ile Asn Ile Arg Arg
50 55 60
Leu Lys Asn Gly Phe Ser Thr Val His Pro Leu Arg Phe Asp Glu Arg
65 70 75 80

Glu Ala Val Glu Arg Trp Thr Gln Glu Arg Ala Asn Trp Lys Gly Ala
85 90 95
Asp Arg Thr Asp Ala Ile Phe Ile Ser Arg Arg Gly Ser Arg Leu Ser
100 105 110
Arg Gln Gln Ala Tyr Arg Ile Ile Arg Asp Ala Gly Ile Glu Ala Gly
115 120 125
Thr Val Thr Gln Thr His Pro His Met Leu Arg His Ala Cys Gly Tyr
130 135 140
Glu Leu Ala Glu Arg Gly Ala Asp Thr Arg Leu Ile Gln Asp Tyr Leu
145 150 155 160
Gly His Arg Asn Ile Arg His Thr Val Arg Tyr Thr Ala Ser Asn Ala
165 170 175
Ala Arg Phe Ala Gly Leu Trp Gly Arg Asn Asn Leu Ile Asn Glu Lys
180 185 190
Leu Lys Arg Gln Glu Val
195

<211> 961
<211> 183
<212> PRT
<213> E. Coli

<400> 361
Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
1 5 10 15
Ser Ser Thr Ala Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr
20 25 30
Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
35 40 45
Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
50 55 60
Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
65 70 75 80
Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
85 90 95
Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
100 105 110
Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
115 120 125
Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
130 135 140
Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
145 150 155 160
Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr
165 170 175
Phe Lys Val Gln Tyr Gln
180

<211> 362
<211> 215
<212> PRT
<213> E. Coli

<400> 362

Met Leu Leu Met Arg Met Arg Pro Ser Arg Phe Ser Ile Asn Asn Leu
1 5 10 15
Pro Arg Phe Arg Asp Val Ile Thr Gly Arg Asp Ala His Pro Cys Ala
20 25 30
Ile Lys Ile Thr Met Lys Arg Lys Arg Leu Phe Leu Leu Ala Ser Leu
35 40 45
Leu Pro Met Phe Ala Leu Ala Gly Asn Lys Trp Asn Thr Thr Leu Pro
50 55 60
Gly Gly Asn Met Gln Phe Gln Gly Val Ile Ile Ala Glu Thr Cys Arg
65 70 75 80
Ile Glu Ala Gly Asp Lys Gln Met Thr Val Asn Met Gly Gln Ile Ser
85 90 95
Ser Asn Arg Phe His Ala Val Gly Glu Asp Ser Ala Pro Val Pro Phe
100 105 110
Val Ile His Leu Arg Glu Cys Ser Thr Val Val Ser Glu Arg Val Gly
115 120 125
Val Ala Phe His Gly Val Ala Asp Gly Lys Asn Pro Asp Val Leu Ser
130 135 140
Val Gly Glu Gly Pro Gly Ile Ala Thr Asn Ile Gly Val Ala Leu Phe
145 150 155 160
Asp Asp Glu Gly Asn Leu Val Pro Ile Asn Arg Pro Pro Ala Asn Trp
165 170 175
Lys Arg Leu Tyr Ser Gly Ser Thr Ser Leu His Phe Ile Ala Lys Tyr
180 185 190
Arg Ala Thr Gly Arg Arg Val Thr Gly Gly Ile Ala Asn Ala Gln Ala
195 200 205
Trp Phe Ser Leu Thr Tyr Gln
210 215

<210> 6
<211> 41
<212> PRT
<213> E. Coli

<400> 6
Met Ser Asn Lys Asn Val Asn Val Arg Lys Ser Gln Glu Ile Thr Phe
1 5 10 15
Cys Leu Leu Ala Gly Ile Leu Met Phe Met Ala Met Met Val Ala Gly
20 25 30
Arg Ala Gln Ala Gly Val Ala Leu Gly Ala Thr Arg Val Ile Tyr Pro
35 40 45
Ala Gly Gln Lys Gln Glu Gln Leu Ala Val Thr Asn Asn Asp Glu Asn
50 55 60
Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys
65 70 75 80
Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys
85 90 95
Lys Gln Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro
100 105 110
Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser
115 120 125
Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile
130 135 140
Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro
145 150 155 160

Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu
165 170 175
Thr Leu Ile Asn Pro Thr Pro Tyr Tyr Leu Thr Val Thr Glu Leu Asn
180 185 190
Ala Gly Thr Arg Val Leu Glu Asn Ala Leu Val Pro Pro Met Gly Glu
195 200 205
Ser Thr Val Lys Leu Pro Ser Asp Ala Gly Ser Asn Ile Thr Tyr Arg
210 215 220
Thr Ile Asn Asp Tyr Gly Ala Leu Thr Pro Lys Met Thr Gly Val Met
225 230 235 240
Glu

(210) 364
(211) 678
(212) PRT
(213) E. Coli

(400) 364
Met Ser Tyr Leu Asn Leu Arg Leu Tyr Gln Arg Asn Thr Gln Cys Leu
1 5 10 15
His Ile Arg Lys His Arg Leu Ala Gly Phe Phe Val Arg Leu Val Val
20 25 30
Ala Cys Ala Phe Ala Ala Gln Ala Pro Leu Ser Ser Ala Asp Leu Tyr
35 40 45
Phe Asn Pro Arg Phe Leu Ala Asp Asp Pro Gln Ala Val Ala Asp Leu
50 55 60
Ser Arg Phe Glu Asn Gly Gln Glu Leu Pro Pro Gly Thr Tyr Arg Val
65 70 75 80
Asp Ile Tyr Leu Asn Asn Gly Tyr Met Ala Thr Arg Asp Val Thr Phe
85 90 95
Asn Thr Gly Asp Ser Glu Gln Gly Ile Val Pro Cys Leu Thr Arg Ala
100 105 110
Gln Leu Ala Ser Met Gly Leu Asn Thr Ala Ser Val Ala Gly Met Asn
115 120 125
Leu Leu Ala Asp Asp Ala Cys Val Pro Leu Thr Thr Met Val Gln Asp
130 135 140
Ala Thr Ala His Leu Asp Val Gly Gln Gln Arg Leu Asn Leu Thr Ile
145 150 155 160
Pro Gln Ala Phe Met Ser Asn Arg Ala Arg Gly Tyr Ile Pro Pro Glu
165 170 175
Leu Trp Asp Pro Gly Ile Asn Ala Gly Leu Leu Asn Tyr Asn Phe Ser
180 185 190
Gly Asn Ser Val Gln Asn Arg Ile Gly Gly Asn Ser His Tyr Ala Tyr
195 200 205
Leu Asn Leu Gln Ser Gly Leu Asn Ile Gly Ala Trp Arg Leu Arg Asp
210 215 220
Asn Thr Thr Trp Ser Tyr Asn Ser Ser Asp Arg Ser Ser Gly Ser Lys
225 230 235 240
Asn Lys Trp Gln His Ile Asn Thr Trp Leu Glu Arg Asp Ile Ile Pro
245 250 255
Leu Arg Ser Arg Leu Thr Leu Gly Asp Gly Tyr Thr Gln Gly Asp Ile
260 265 270
Phe Asp Gly Ile Asn Phe Arg Gly Ala Gln Leu Ala Ser Asp Asp Asn
275 280 285
Met Leu Pro Asp Ser Gln Arg Gly Phe Ala Pro Val Ile His Gly Ile

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                290                 295                 300
Ala Arg Gly Thr Ala Gln Val Thr Ile Lys Gln Asn Gly Tyr Asp Ile
305                 310                 315                 320
Tyr Asn Ser Thr Val Pro Pro Gly Pro Phe Thr Ile Asn Asp Ile Tyr
                325                 330                 335
Ala Ala Gly Asn Ser Gly Asp Leu Gln Val Thr Ile Lys Glu Ala Asp
            340                 345                 350
Gly Ser Thr Gln Ile Phe Thr Val Pro Tyr Ser Ser Val Pro Leu Leu
        355                 360                 365
Gln Arg Glu Gly His Thr Arg Tyr Ser Ile Thr Ala Gly Glu Tyr Arg
    370                 375                 380
Ser Gly Asn Ala Gln Gln Glu Lys Thr Arg Phe Phe Gln Ser Thr Leu
385                 390                 395                 400
Leu His Gly Leu Pro Ala Gly Trp Thr Ile Tyr Gly Gly Thr Gln Leu
                405                 410                 415
Ala Asp Arg Tyr Arg Ala Phe Asn Phe Gly Ile Gly Lys Asn Met Gly
            420                 425                 430
Ala Leu Gly Ala Leu Ser Val Asp Met Thr Gln Ala Asn Ser Thr Leu
        435                 440                 445
Pro Asp Asp Ser Gln His Asp Gly Gln Ser Val Arg Phe Leu Tyr Asn
    450                 455                 460
Lys Ser Leu Asn Glu Ser Gly Thr Asn Ile Gln Leu Val Gly Tyr Arg
465                 470                 475                 480
Tyr Ser Thr Ser Gly Tyr Pro Asn Phe Ala Asp Thr Thr Tyr Ser Arg
                485                 490                 495
Met Asn Gly Tyr Asn Ile Glu Thr Gln Asp Gly Val Ile Gln Val Lys
            500                 505                 510
Pro Lys Phe Thr Asp Tyr Tyr Asn Leu Ala Tyr Asn Lys Arg Gly Lys
        515                 520                 525
Leu Gln Leu Thr Val Thr Gln Gln Leu Gly Arg Thr Ser Thr Leu Tyr
    530                 535                 540
Leu Ser Gly Ser His Gln Thr Tyr Trp Gly Thr Ser Asn Val Asp Glu
545                 550                 555                 560
Gln Phe Gln Ala Gly Leu Asn Thr Ala Phe Glu Asp Ile Asn Trp Thr
                565                 570                 575
Leu Ser Tyr Ser Leu Thr Lys Asn Ala Trp Gln Lys Gly Arg Asp Gln
            580                 585                 590
Met Leu Ala Leu Asn Val Asn Ile Pro Phe Ser His Trp Leu Arg Ser
        595                 600                 605
Asp Ser Lys Ser Gln Trp Arg His Ala Ser Ala Ser Tyr Ser Met Ser
    610                 615                 620
His Asp Leu Asn Gly Arg Met Thr Asn Leu Ala Gly Val Tyr Gly Thr
625                 630                 635                 640
Leu Leu Gln Asp Asn Asn Leu Ser Tyr Ser Val Gln Thr Gly Tyr Ala
                645                 650                 655
Gly Gly Gly Asp Gly Asn Ser Gly Ser Thr Gly Tyr Ala Thr Leu Asn
            660                 665                 670
Tyr Arg Gly Gly Tyr Gly Asn Ala Asn Ile Gly Tyr Ser His Ser Asp
        675                 680                 685
Asp Ile Lys Gln Leu Tyr Tyr Gly Val Ser Gly Gly Val Leu Ala His
    690                 695                 700
Ala Asn Gly Val Thr Leu Gly Gln Pro Leu Asn Asp Thr Val Val Leu
705                 710                 715                 720
Val Lys Ala Pro Gly Ala Lys Asp Ala Lys Val Glu Asn Gln Thr Gly
                725                 730                 735
Val Arg Thr Asp Trp Arg Gly Tyr Ala Val Leu Pro Tyr Ala Thr Glu
            740                 745                 750
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Tyr Arg Glu Asn Arg Val Ala Leu Asp Thr Asn Thr Leu Ala Asp Asn
755 760 765
Val Asp Leu Asp Asn Ala Val Ala Asn Val Val Pro Thr Arg Gly Ala
770 775 780
Ile Val Arg Ala Glu Phe Lys Ala Arg Val Gly Ile Lys Leu Leu Met
785 790 795 800
Thr Leu Thr His Asn Asn Lys Pro Leu Pro Phe Gly Ala Met Val Thr
805 810 815
Ser Glu Ser Ser Gln Ser Ser Gly Ile Val Ala Asp Asn Gly Gln Val
820 825 830
Tyr Leu Ser Gly Met Pro Leu Ala Gly Lys Val Gln Val Lys Trp Gly
835 840 845
Glu Glu Glu Asn Ala His Cys Val Ala Asn Tyr Gln Leu Pro Pro Glu
850 855 860
Ser Gln Gln Gln Leu Leu Thr Gln Leu Ser Ala Glu Cys Arg
865 870 875

<210> 365
<211> 176
<212> PRT
<213> E. Coli

<400> 365
Met Arg Asn Lys Pro Phe Tyr Leu Leu Cys Ala Phe Leu Trp Leu Ala
1 5 10 15
Val Ser His Ala Leu Ala Ala Asp Ser Thr Ile Thr Ile Arg Gly Tyr
20 25 30
Val Arg Asp Asn Gly Cys Ser Val Ala Ala Glu Ser Thr Asn Pro Thr
35 40 45
Val Asp Leu Met Glu Asn Ala Ala Lys Gln Phe Asn Asn Ile Gly Ala
50 55 60
Thr Thr Pro Val Val Pro Phe Arg Ile Leu Leu Ser Pro Cys Gly Asn
65 70 75 80
Ala Val Ser Ala Val Lys Val Gly Phe Thr Gly Val Ala Asp Ser His
85 90 95
Asn Ala Asn Leu Leu Ala Leu Glu Asn Thr Val Ser Ala Ala Ser Gly
100 105 110
Leu Gly Ile Gln Leu Leu Asn Glu Gln Gln Asn Gln Ile Pro Leu Asn
115 120 125
Ala Pro Ser Ser Ala Leu Ser Trp Thr Thr Leu Thr Pro Gly Lys Pro
130 135 140
Asn Thr Leu Asn Phe Tyr Ala Arg Leu Met Ala Thr Gln Val Pro Val
145 150 155 160
Thr Ala Gly His Ile Asn Ala Thr Ala Thr Phe Thr Leu Glu Tyr Gln
165 170 175

<210> 366
<211> 167
<212> PRT
<213> E. Coli

<400> 366
Met Lys Trp Cys Lys Arg Gly Tyr Val Leu Ala Ala Ile Leu Ala Leu
1 5 10 15

Ala Ser Ala Thr Ile Gln Ala Ala Asp Val Thr Ile Thr Val Asn Gly
20 25 30

Lys Val Val Ala Lys Pro Cys Thr Val Ser Thr Thr Asn Ala Thr Val
35 40 45

Asp Leu Gly Asp Leu Tyr Ser Phe Ser Leu Met Ser Ala Gly Ala Ala
50 55 60

Ser Ala Trp His Asp Val Ala Leu Glu Leu Thr Asn Cys Pro Val Gly
65 70 75 80

Thr Ser Arg Val Thr Ala Ser Phe Ser Gly Ala Ala Asp Ser Thr Gly
85 90 95

Tyr Tyr Lys Asn Gln Gly Thr Ala Gln Asn Ile Gln Leu Glu Leu Gln
100 105 110

Asp Asp Ser Gly Asn Thr Leu Asn Thr Gly Ala Thr Lys Thr Val Gln
115 120 125

Val Asp Asp Ser Ser Gln Ser Ala His Phe Pro Leu Gln Val Arg Ala
130 135 140

Leu Thr Val Asn Gly Gly Ala Thr Gln Gly Thr Ile Gln Ala Val Ile
145 150 155 160

Ser Ile Thr Tyr Thr Tyr Ser
165

<210> 367

<211> 300

<212> PRT

<213> E. Coli

<400> 367

Met Lys Arg Val Ile Thr Leu Phe Ala Val Leu Leu Met Gly Trp Ser
1 5 10 15

Val Asn Ala Trp Ser Phe Ala Cys Lys Thr Ala Asn Gly Thr Ala Ile
20 25 30

Pro Ile Gly Gly Gly Ser Ala Asn Val Tyr Val Asn Leu Ala Pro Val
35 40 45

Val Asn Val Gly Gln Asn Leu Val Val Asp Leu Ser Thr Gln Ile Phe
50 55 60

Cys His Asn Asp Tyr Pro Glu Thr Ile Thr Asp Tyr Val Thr Leu Gln
65 70 75 80

Arg Gly Ser Ala Tyr Gly Gly Val Leu Ser Asn Phe Ser Gly Thr Val
85 90 95

Lys Tyr Ser Gly Ser Ser Tyr Pro Phe Pro Thr Thr Ser Glu Thr Pro
100 105 110

Arg Val Val Tyr Asn Ser Arg Thr Asp Lys Pro Trp Pro Val Ala Leu
115 120 125

Tyr Leu Thr Pro Val Ser Ser Ala Gly Gly Val Ala Ile Lys Ala Gly
130 135 140

Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser
145 150 155 160

Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val
165 170 175

Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr
180 185 190

Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys
195 200 205

Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp
210 215 220

Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln
225 230 235 240
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn
245 250 255
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly
260 265 270
Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn
275 280 285
Val Gln Ser Ile Ile Gly Val Thr Phe Val Tyr Gln
290 295 300

<210> 365
<211> 5.1
<212> PRT
<213> E. Coli

<400> 365
Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys
1 5 10 15
Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu
20 25 30
Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp
35 40 45
Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile
50 55 60
Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn
65 70 75 80
Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu
85 90 95
Ser Asn Asp Ser Arg Leu Thr Gly Cys Glu Arg Ser Pro Phe Glu Ser
100 105 110
Tyr Gly Asn Cys Ser Leu Thr Gly Gln Arg Thr Leu Arg Asn Phe Pro
115 120 125
Gly Cys Arg His Gly Pro Cys Arg Ser Cys Ala Gly Val Leu Gly Ser
130 135 140
Ser Gln Lys Glu Arg Pro Ala Ser Leu Pro Gly Ser Ser Arg Lys Ile
145 150 155 160
Val Arg Lys Ser Val Leu Ser Ala Ala Ser Val Leu Leu Asp Lys Ser
165 170 175
Cys Gln Ala Arg Ala Ser Ser Ser Ile Ser Met Asn Thr Lys Ile Arg
180 185 190
Tyr Gly Leu Ser Ala Ala Val Leu Ala Leu Ile Gly Ala Gly Ala Ser
195 200 205
Ala Pro Gln Ile Leu Asp Gln Phe Leu Asp Glu Lys Glu Gly Asn His
210 215 220
Thr Met Ala Tyr Arg Asp Gly Ser Gly Ile Trp Thr Ile Cys Arg Gly
225 230 235 240
Ala Thr Val Val Asp Gly Lys Thr Val Phe Pro Asn Met Lys Leu Ser
245 250 255
Lys Glu Lys Cys Asp Gln Val Asn Ala Ile Glu Arg Asp Lys Ala Leu
260 265 270
Ala Trp Val Glu Arg Asn Ile Lys Val Pro Leu Thr Glu Pro Gln Lys
275 280 285
Ala Gly Ile Ala Ser Phe Cys Pro Tyr Asn Ile Gly Pro Gly Lys Cys
290 295 300

Phe Pro Ser Thr Phe Tyr Lys Arg Leu Asn Ala Gly Asp Arg Lys Gly
305 310 315 320
Ala Cys Glu Ala Ile Arg Trp Trp Ile Lys Asp Gly Gly Arg Asp Cys
325 330 335
Arg Ile Arg Ser Asn Asn Cys Tyr Gly Gln Val Ile Arg Arg Asp Gln
340 345 350
Glu Ser Ala Leu Thr Cys Trp Gly Ile Glu Gln Ile Arg Tyr Ser Trp
355 360 365
Phe Phe Ser Cys Cys Gln Asp Leu Ser Ser Glu Met Ser Gly Ala Thr
370 375 380
Glu Asp Gly Lys Lys Asn Gly Arg Asn Val Met Leu Pro His Tyr His
385 390 395 400
Lys Arg Met Leu Asn Leu Leu Leu Glu Leu Asn Arg Gly Glu Leu Pro
405 410 415
Val Met Arg Leu Leu Lys Met Arg Asn Arg Asn Leu Leu Lys Phe Leu
420 425 430
Pro Gly Leu Leu Ile Cys Leu Ile Val Leu Thr Ser Cys Val Pro Lys
435 440 445
Gln Lys Asn Met Pro Tyr Ala Leu Thr Gln Arg Ser Ile Pro Glu Ile
450 455 460
Leu Pro Leu Pro Ser Glu Ala Lys Gln Pro Lys Pro Pro Lys Glu Cys
465 470 475 480
Ser Pro Thr Cys Ser Glu Ile Leu Gln Gln Lys Leu Ser Phe Met Leu
485 490 495
Lys Leu Leu Thr Asn Ala Thr Ser Gln Glu Leu Val Asn Arg Ser Met
500 505 510
Asn Leu Glu Ile Lys Ser Ile Lys Cys
515

(213) 364
(211) 1
(212) PRT
(213) E. Coli

(400) 364
Met Asn Thr Lys Ile Arg Tyr Gly Leu Ser Ala Ala Val Leu Ala Leu
1 5 10 15
Ile Gly Ala Gly Ala Ser Ala Pro Gln Ile Leu Asp Gln Phe Leu Asp
20 25 30
Glu Lys Glu Gly Asn His Thr Met Ala Tyr Arg Asp Gly Ser Gly Ile
35 40 45
Trp Thr Ile Cys Arg Gly Ala Thr Val Val Asp Gly Lys Thr Val Phe
50 55 60
Pro Asn Met Lys Leu Ser Lys Glu Lys Cys Asp Gln Val Asn Ala Ile
65 70 75 80
Glu Arg Asp Lys Ala Leu Ala Trp Val Glu Arg Asn Ile Lys Val Pro
85 90 95
Leu Thr Gln Pro Gln Lys Ala Gly Ile Ala Ser Phe Cys Pro Tyr Asn
100 105 110
Ile Gly Pro Gly Lys Cys Phe Pro Ser Thr Phe Tyr Lys Arg Leu Asn
115 120 125
Ala Gly Asp Arg Lys Gly Ala Cys Glu Ala Ile Arg Trp Trp Ile Lys
130 135 140
Asp Gly Gly Arg Asp Cys Arg Ile Arg Ser Asn Asn Cys Tyr Gly Gln
145 150 155 160

Val Ile Arg Arg Asp Gln Glu Ser Ala Leu Thr Cys Trp Gly Ile Glu
165 170 175
Gln

<210> 370
<211> 103
<212> PRT
<213> E. Coli

<400> 370
Met Thr Gln Asp Tyr Glu Leu Val Val Lys Gly Val Arg Asn Phe Glu
1 5 10 15
Asn Lys Val Thr Val Thr Val Ala Leu Gln Asp Lys Glu Arg Phe Asp
20 25 30
Gly Glu Ile Phe Asp Leu Asp Val Ala Met Asp Arg Val Glu Gly Ala
35 40 45
Ala Leu Glu Phe Tyr Glu Ala Ala Ala Arg Arg Ser Val Arg Gln Val
50 55 60
Phe Leu Glu Val Ala Glu Lys Leu Ser Glu Lys Val Glu Ser Tyr Leu
65 70 75 80
Gln His Gln Tyr Ser Phe Lys Ile Glu Asn Pro Ala Asn Lys His Glu
85 90 95
Arg Pro His His Lys Tyr Leu
100

<210> 371
<211> 97
<212> PRT
<213> E. Coli

<400> 371
Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys
1 5 10 15
Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu
20 25 30
Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp
35 40 45
Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile
50 55 60
Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn
65 70 75 80
Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu
85 90 95

<210> 372
<211> 71
<212> PRT
<213> E. Coli

<400> 372
Met Ser Asn Lys Met Thr Gly Leu Val Lys Trp Phe Asn Ala Asp Lys

```
 1               5                  10                  15
Gly Phe Gly Phe Ile Ser Pro Val Asp Gly Ser Lys Asp Val Phe Val
            20                  25                  30
His Phe Ser Ala Ile Gln Asn Asp Asn Tyr Arg Thr Leu Phe Glu Gly
        35                  40                  45
Gln Lys Val Thr Phe Ser Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
    50                  55                  60
Ala Asn Val Ile Ile Thr Asp
65                  70
```

<210> 373
<211> 436
<212> PRT
<213> E. Coli

<400> 373

```
Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln
 1               5                  10                  15
Leu Thr Pro Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg
            20                  25                  30
Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn
        35                  40                  45
Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg
    50                  55                  60
Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His
65                  70                  75                  80
Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile
                85                  90                  95
Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro
            100                 105                 110
Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln
        115                 120                 125
Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala
    130                 135                 140
Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu
145                 150                 155                 160
Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met
                165                 170                 175
His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His
            180                 185                 190
Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr
        195                 200                 205
Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly
    210                 215                 220
Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln
225                 230                 235                 240
Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg
                245                 250                 255
Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr
            260                 265                 270
Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu
        275                 280                 285
His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg
    290                 295                 300
Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr
```

305 310 315 320
Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg
325 330 335
Ser His

(210) 374
(211) 157
(212) PRT
(213) E. Coli

(400) 374
Met Val Tyr Ile Ile Ile Val Ser His Gly His Glu Asp Tyr Ile Lys
1 5 10 15
Lys Leu Leu Glu Asn Leu Asn Ala Asp Asp Glu His Tyr Lys Ile Ile
20 25 30
Val Arg Asp Asn Lys Asp Ser Leu Leu Leu Lys Gln Ile Cys Gln His
35 40 45
Tyr Ala Gly Leu Asp Tyr Ile Ser Gly Gly Val Tyr Gly Phe Gly His
50 55 60
Asn Asn Asn Ile Ala Val Ala Tyr Val Lys Glu Lys Tyr Arg Pro Ala
65 70 75 80
Asp Asp Asp Tyr Ile Leu Phe Leu Asn Pro Asp Ile Ile Met Lys His
85 90 95
Asp Asp Leu Leu Thr Tyr Ile Lys Tyr Val Glu Ser Lys Arg Tyr Ala
100 105 110
Phe Ser Thr Leu Cys Leu Phe Arg Asp Glu Ala Lys Ser Leu His Asp
115 120 125
Tyr Ser Val Arg Lys Phe Pro Val Leu Ser Asp Phe Ile Val Ser Phe
130 135 140
Met Leu Gly Ile Lys Glu Gly Ala Asn Lys Ser Leu Ile
145 150 155

(210) 375
(211) 372
(212) PRT
(213) E. Coli

(400) 375
Met Gly Lys Ser Ile Val Val Val Ser Ala Val Asn Phe Thr Thr Gly
1 5 10 15
Gly Pro Phe Thr Ile Leu Lys Lys Phe Leu Ala Ala Thr Asn Asn Lys
20 25 30
Glu Asn Val Ser Phe Ile Ala Leu Val His Ser Ala Lys Glu Leu Lys
35 40 45
Glu Ser Tyr Pro Trp Val Lys Phe Ile Glu Phe Pro Glu Val Lys Gly
50 55 60
Ser Trp Leu Lys Arg Leu His Phe Glu Tyr Val Val Cys Lys Lys Leu
65 70 75 80
Ser Lys Glu Leu Asn Ala Thr His Trp Ile Cys Leu His Asp Ile Thr
85 90 95
Ala Asn Val Val Thr Lys Lys Arg Tyr Val Tyr Cys His Asn Pro Ala
100 105 110
Pro Phe Tyr Lys Gly Ile Leu Phe Arg Glu Ile Leu Met Glu Pro Ser

```
        115                 120                 125
Phe Phe Leu Phe Lys Met Leu Tyr Gly Leu Ile Tyr Lys Ile Asn Ile
    130                 135                 140
Lys Lys Asn Thr Ala Val Phe Val Gln Gln Phe Trp Met Lys Glu Lys
145                 150                 155                 160
Phe Ile Lys Lys Tyr Ser Ile Asn Asn Ile Ile Val Ser Arg Pro Glu
                165                 170                 175
Ile Lys Leu Ser Asp Lys Ser Gln Leu Thr Asp Asp Asp Ser Gln Phe
            180                 185                 190
Lys Asn Asn Pro Ser Glu Leu Thr Ile Phe Tyr Pro Ala Val Pro Arg
        195                 200                 205
Val Phe Lys Asn Tyr Glu Leu Ile Ile Ser Ala Ala Arg Lys Leu Lys
    210                 215                 220
Glu Gln Ser Asn Ile Lys Phe Leu Leu Thr Ile Ser Gly Thr Glu Asn
225                 230                 235                 240
Ala Tyr Ala Lys Tyr Ile Ile Ser Leu Ala Glu Gly Leu Asp Asn Val
                245                 250                 255
His Phe Leu Gly Tyr Leu Asp Lys Glu Lys Ile Asp His Cys Tyr Asn
            260                 265                 270
Ile Ser Asp Ile Val Cys Phe Pro Ser Arg Leu Glu Thr Trp Gly Leu
        275                 280                 285
Pro Leu Ser Glu Ala Lys Glu Arg Gly Lys Trp Val Leu Ala Ser Asp
    290                 295                 300
Phe Pro Phe Thr Arg Glu Thr Leu Gly Ser Tyr Glu Lys Lys Ala Phe
305                 310                 315                 320
Phe Asp Ser Asn Asn Asp Asp Met Leu Val Lys Leu Ile Ile Asp Phe
                325                 330                 335
Lys Lys Gly Asn Leu Lys Lys Asp Ile Ser Asp Ala Asn Phe Ile Tyr
            340                 345                 350
Arg Asn Glu Asn Val Leu Val Gly Phe Asp Glu Leu Val Asn Phe Ile
        355                 360                 365
Thr Glu Glu His
    370
```


<210> 376
<211> 196
<212> PRT
<213> E. Coli

<400> 376


```
Met Ile Leu Lys Leu Ala Lys Arg Tyr Gly Leu Cys Gly Phe Ile Arg
 1               5                  10                  15
Leu Val Arg Asp Val Leu Leu Thr Arg Val Phe Tyr Arg Asn Cys Arg
            20                  25                  30
Ile Ile Arg Phe Pro Cys Tyr Ile Arg Asn Asp Gly Ser Ile Asn Phe
        35                  40                  45
Gly Glu Asn Phe Thr Ser Gly Val Gly Leu Arg Leu Asp Ala Phe Gly
    50                  55                  60
Arg Gly Val Ile Phe Phe Ser Asp Asn Val Gln Val Asn Asp Tyr Val
65                  70                  75                  80
His Ile Ala Ser Ile Glu Ser Val Thr Ile Gly Arg Asp Thr Leu Ile
                85                  90                  95
Ala Ser Lys Val Phe Ile Thr Asp His Asn His Gly Ser Phe Lys His
            100                 105                 110
Ser Asp Pro Met Ser Ser Pro Asn Ile Pro Pro Asp Met Arg Thr Leu
        115                 120                 125
```

Glu Ser Ser Ala Val Val Ile Gly Gln Arg Val Trp Leu Gly Glu Asn
130 135 140
Val Thr Val Leu Pro Gly Thr Ile Ile Gly Asn Gly Val Val Val Gly
145 150 155 160
Ala Asn Ser Val Val Arg Gly Ser Ile Pro Glu Asn Thr Val Ile Ala
165 170 175
Gly Val Pro Ala Lys Ile Ile Lys Lys Tyr Asn His Glu Thr Lys Leu
180 185 190
Trp Glu Lys Ala
195

<210> 377
<211> 330
<212> PRT
<213> E. Coli

<400> 377
Met Tyr Phe Leu Asn Asp Leu Asn Phe Ser Arg Arg Asp Ala Gly Phe
1 5 10 15
Lys Ala Asn Lys Asp Ala Leu Asp Ile Ala Ser Asp Tyr Glu Asn Ile
20 25 30
Ser Val Val Asn Ile Pro Leu Trp Gly Gly Val Val Gln Arg Ile Ile
35 40 45
Ser Ser Val Lys Leu Ser Thr Phe Leu Cys Gly Leu Glu Asn Lys Asp
50 55 60
Val Leu Ile Phe Asn Phe Pro Met Ala Lys Pro Phe Trp His Ile Leu
65 70 75 80
Ser Phe Phe His Arg Leu Leu Lys Phe Arg Ile Val Pro Leu Ile His
85 90 95
Asp Ile Asp Glu Leu Arg Gly Gly Gly Gly Ser Asp Ser Val Arg Leu
100 105 110
Ala Thr Cys Asp Met Val Ile Ser His Asn Pro Gln Met Thr Lys Tyr
115 120 125
Leu Ser Lys Tyr Met Ser Gln Asp Lys Ile Lys Asp Ile Lys Ile Phe
130 135 140
Asp Tyr Leu Val Ser Ser Asp Val Glu His Arg Asp Val Thr Asp Lys
145 150 155 160
Gln Arg Gly Val Ile Tyr Ala Gly Asn Leu Ser Arg His Lys Cys Ser
165 170 175
Phe Ile Tyr Thr Glu Gly Cys Asp Phe Thr Leu Phe Gly Val Asn Tyr
180 185 190
Glu Asn Lys Asp Asn Pro Lys Tyr Leu Gly Ser Phe Asp Ala Gln Ser
195 200 205
Pro Glu Lys Ile Asn Leu Pro Gly Met Gln Phe Gly Leu Ile Trp Asp
210 215 220
Gly Asp Ser Val Glu Thr Cys Ser Gly Ala Phe Gly Asp Tyr Leu Lys
225 230 235 240
Phe Asn Asn Pro His Lys Thr Ser Leu Tyr Leu Ser Met Glu Leu Pro
245 250 255
Val Phe Ile Trp Asp Lys Ala Ala Leu Ala Asp Phe Ile Val Asp Asn
260 265 270
Arg Ile Gly Tyr Ala Val Gly Ser Ile Lys Glu Met Gln Glu Ile Val
275 280 285
Asp Ser Met Thr Ile Glu Thr Tyr Lys Gln Ile Ser Glu Asn Thr Lys
290 295 300
Ile Ile Ser Gln Lys Ile Arg Thr Gly Ser Tyr Phe Arg Asp Val Leu
305 310 315 320

Glu Glu Val Ile Asp Asp Leu Lys Thr Arg
305 310

(210) 378
(211) 393
(212) PRT
(213) E. Coli

(400) 378

Met Ile Tyr Leu Val Ile Ser Val Phe Leu Ile Thr Ala Phe Ile Cys
1 5 10 15
Leu Tyr Leu Lys Lys Asp Ile Phe Tyr Pro Ala Val Cys Val Asn Ile
20 25 30
Ile Phe Ala Leu Val Leu Leu Gly Tyr Glu Ile Thr Ser Asp Ile Tyr
35 40 45
Ala Phe Gln Leu Asn Asp Ala Thr Leu Ile Phe Leu Leu Cys Asn Val
50 55 60
Leu Thr Phe Thr Leu Ser Cys Leu Leu Thr Glu Ser Val Leu Asp Leu
65 70 75 80
Asn Ile Asn Lys Val Asn Asn Ala Ile Tyr Ser Ile Pro Ser Lys Lys
85 90 95
Val His Asn Val Gly Leu Leu Val Ile Ser Phe Ser Met Ile Tyr Ile
100 105 110
Cys Met Asn Leu Ser Asn Tyr Gln Phe Gly Thr Ser Leu Leu Ser Tyr
115 120 125
Met Asn Leu Ile Arg Asp Ala Asp Val Glu Asp Thr Ser Arg Asn Phe
130 135 140
Ser Ala Tyr Met Gln Pro Ile Ile Leu Thr Thr Phe Ala Leu Phe Ile
145 150 155 160
Trp Ser Lys Lys Phe Thr Asn Thr Lys Val Ser Lys Thr Phe Thr Leu
165 170 175
Leu Val Phe Ile Val Phe Ile Phe Ala Ile Ile Leu Asn Thr Gly Lys
180 185 190
Gln Ile Val Phe Met Val Ile Ile Ser Tyr Ala Phe Ile Val Gly Val
195 200 205
Asn Arg Val Lys His Tyr Val Tyr Leu Ile Thr Ala Val Gly Val Leu
210 215 220
Phe Ser Leu Tyr Met Leu Phe Leu Arg Gly Leu Pro Gly Gly Met Ala
225 230 235 240
Tyr Tyr Leu Ser Met Tyr Leu Val Ser Pro Ile Ile Ala Phe Gln Glu
245 250 255
Phe Tyr Phe Gln Gln Val Ser Asn Ser Ala Ser Ser His Val Phe Trp
260 265 270
Phe Phe Glu Arg Leu Met Gly Leu Leu Thr Gly Gly Val Ser Met Ser
275 280 285
Leu His Lys Glu Phe Val Trp Val Gly Leu Pro Thr Asn Val Tyr Thr
290 295 300
Ala Phe Ser Asp Tyr Val Tyr Ile Ser Ala Glu Leu Ser Tyr Leu Met
305 310 315 320
Met Val Ile His Gly Cys Ile Ser Gly Val Leu Trp Arg Leu Ser Arg
325 330 335
Asn Tyr Ile Ser Val Lys Ile Phe Tyr Ser Tyr Phe Ile Tyr Thr Phe
340 345 350
Ser Phe Ile Phe Tyr His Glu Ser Phe Met Thr Asn Ile Ser Ser Trp
355 360 365
Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala

370 375 380

Gln Lys Ile Lys
385

<210> 379
<211> 367
<212> PRT
<213> E. Coli

<400> 379

Met Tyr Asp Tyr Ile Ile Val Gly Ser Gly Leu Phe Gly Ala Val Cys
1 5 10 15

Ala Asn Glu Leu Lys Lys Leu Asn Lys Lys Val Leu Val Ile Glu Lys
20 25 30

Arg Asn His Ile Gly Gly Asn Ala Tyr Thr Glu Asp Cys Glu Gly Ile
35 40 45

Gln Ile His Lys Tyr Gly Ala His Ile Phe His Thr Asn Asp Lys Tyr
50 55 60

Ile Trp Asp Tyr Val Asn Asp Leu Val Glu Phe Asn Arg Phe Thr Asn
65 70 75 80

Ser Pro Leu Ala Ile Tyr Lys Asp Lys Leu Phe Asn Leu Pro Phe Asn
85 90 95

Met Asn Thr Phe His Gln Met Trp Gly Val Lys Asp Pro Gln Glu Ala
100 105 110

Gln Asn Ile Ile Asn Ala Gln Lys Lys Lys Tyr Gly Asp Lys Val Pro
115 120 125

Glu Asn Leu Glu Glu Gln Ala Ile Ser Leu Val Gly Glu Asp Leu Tyr
130 135 140

Gln Ala Leu Ile Lys Gly Tyr Thr Glu Lys Gln Trp Gly Arg Ser Ala
145 150 155 160

Lys Glu Leu Pro Ala Phe Ile Ile Lys Arg Ile Pro Val Arg Phe Thr
165 170 175

Phe Asp Asn Asn Tyr Phe Ser Asp Arg Tyr Gln Gly Ile Pro Val Gly
180 185 190

Gly Tyr Thr Lys Leu Ile Glu Lys Met Leu Glu Gly Val Asp Val Lys
195 200 205

Leu Gly Ile Asp Phe Leu Lys Asp Lys Asp Ser Leu Ala Ser Lys Ala
210 215 220

His Arg Ile Ile Tyr Thr Gly Pro Ile Asp Gln Tyr Phe Asp Tyr Arg
225 230 235 240

Phe Gly Ala Leu Glu Tyr Arg Ser Leu Lys Phe Glu Thr Glu Arg His
245 250 255

Glu Phe Pro Asn Phe Gln Gly Asn Ala Val Ile Asn Phe Thr Asp Ala
260 265 270

Asn Val Pro Tyr Thr Arg Ile Ile Glu His Lys His Phe Asp Tyr Val
275 280 285

Glu Thr Lys His Thr Val Val Thr Lys Glu Tyr Pro Leu Glu Trp Lys
290 295 300

Val Gly Asp Glu Pro Tyr Tyr Pro Val Asn Asp Asn Lys Asn Met Glu
305 310 315 320

Leu Phe Lys Lys Tyr Arg Glu Leu Ala Ser Arg Glu Asp Lys Val Ile
325 330 335

Phe Gly Gly Arg Leu Ala Glu Tyr Lys Tyr Tyr Asp Met His Gln Val
340 345 350

Ile Ser Ala Ala Leu Tyr Gln Val Lys Asn Ile Met Ser Thr Asp

355 360 365

<210> 480
<211> 371
<212> PRT
<213> E. Coli

<400> 480

Met Phe Pro Lys Ile Met Asn Asp Glu Asn Phe Phe Lys Lys Ala Ala
1 5 10 15
Ala His Gly Glu Glu Pro Pro Leu Thr Pro Gln Asn Glu His Gln Arg
20 25 30
Ser Gly Leu Arg Phe Ala Arg Arg Val Arg Leu Pro Arg Ala Val Gly
35 40 45
Leu Ala Gly Met Phe Leu Pro Ile Ala Ser Thr Leu Val Ser His Pro
50 55 60
Pro Pro Gly Trp Trp Trp Leu Val Leu Val Gly Trp Ala Phe Val Trp
65 70 75 80
Pro His Leu Ala Trp Gln Ile Ala Ser Arg Ala Val Asp Pro Leu Ser
85 90 95
Arg Glu Ile Tyr Asn Leu Lys Thr Asp Ala Val Leu Ala Gly Met Trp
100 105 110
Val Gly Val Met Gly Val Asn Val Leu Pro Ser Thr Ala Met Leu Met
115 120 125
Ile Met Cys Leu Asn Leu Met Gly Ala Gly Gly Pro Arg Leu Phe Val
130 135 140
Ala Gly Leu Val Leu Met Val Val Ser Cys Leu Val Thr Leu Glu Leu
145 150 155 160
Thr Gly Ile Thr Val Ser Phe Asn Ser Ala Pro Leu Glu Trp Trp Leu
165 170 175
Ser Leu Pro Ile Ile Val Ile Tyr Pro Leu Leu Phe Gly Trp Val Ser
180 185 190
Tyr Gln Thr Ala Thr Lys Leu Ala Glu His Lys Arg Arg Leu Gln Val
195 200 205
Met Ser Thr Arg Asp Gly Met Thr Gly Val Tyr Asn Arg Arg His Trp
210 215 220
Glu Thr Met Leu Arg Asn Glu Phe Asp Asn Cys Arg Arg His Asn Arg
225 230 235 240
Asp Ala Thr Leu Leu Ile Ile Asp Ile Asp His Phe Lys Ser Ile Asn
245 250 255
Asp Thr Trp Gly His Asp Val Gly Asp Glu Ala Ile Val Ala Leu Thr
260 265 270
Arg Gln Leu Gln Ile Thr Leu Arg Gly Ser Asp Val Ile Gly Arg Phe
275 280 285
Gly Gly Asp Glu Phe Ala Val Ile Met Ser Gly Thr Pro Ala Glu Ser
290 295 300
Ala Ile Thr Ala Met Leu Arg Val His Glu Gly Leu Asn Thr Leu Arg
305 310 315 320
Leu Pro Asn Thr Pro Gln Val Thr Leu Arg Ile Ser Val Gly Val Ala
325 330 335
Pro Leu Asn Pro Gln Met Ser His Tyr Arg Glu Trp Leu Lys Ser Ala
340 345 350
Asp Leu Ala Leu Tyr Lys Ala Lys Lys Ala Gly Arg Asn Arg Thr Glu
355 360 365
Val Ala Ala
370

<210> 381
<211> 467
<212> PRT
<213> E. Coli

<400> 381

Met	Asp	Val	Asn	Val	Asp	Gln	Phe	Asp	Thr	Glu	Ala	Phe	Arg	Thr	Asp
1				5					10					15	
Lys	Leu	Glu	Leu	Thr	Ser	Gly	Asn	Ile	Ala	Asp	His	Asn	Gly	Asn	Val
			20					25					30		
Val	Ser	Gly	Val	Phe	Asp	Ile	His	Ser	Ser	Asp	Tyr	Val	Leu	Asn	Ala
		35					40					45			
Asp	Leu	Val	Asn	Asp	Arg	Thr	Trp	Asp	Thr	Ser	Lys	Ser	Asn	Tyr	Gly
	50					55					60				
Tyr	Gly	Ile	Val	Ala	Met	Asn	Ser	Asp	Gly	His	Leu	Thr	Ile	Asn	Gly
65					70					75					80
Asn	Gly	Asp	Val	Asp	Asn	Gly	Thr	Glu	Leu	Asp	Asn	Ser	Ser	Val	Asp
				85					90					95	
Asn	Val	Val	Ala	Ala	Thr	Gly	Asn	Tyr	Lys	Val	Arg	Ile	Asp	Asn	Ala
			100					105					110		
Thr	Gly	Ala	Gly	Ala	Ile	Ala	Asp	Tyr	Lys	Asp	Lys	Glu	Ile	Ile	Tyr
		115					120					125			
Val	Asn	Asp	Val	Asn	Ser	Asn	Ala	Thr	Phe	Ser	Ala	Ala	Asn	Lys	Ala
	130					135					140				
Asp	Leu	Gly	Ala	Tyr	Thr	Tyr	Gln	Ala	Glu	Gln	Arg	Gly	Asn	Thr	Val
145					150					155					160
Val	Leu	Gln	Gln	Met	Gln	Leu	Thr	Asp	Tyr	Ala	Asn	Ser	Ala	Leu	Ser
				165					170					175	
Ile	Pro	Ser	Ala	Asn	Thr	Asn	Ile	Trp	Asn	Leu	Glu	Gln	Asp	Thr	Val
			180					185					190		
Gly	Thr	Arg	Leu	Thr	Asn	Ser	Arg	His	Gly	Leu	Ala	Asp	Asn	Gly	Gly
		195					200					205			
Ala	Trp	Val	Ser	Tyr	Phe	Gly	Gly	Asn	Phe	Asn	Gly	Asp	Asn	Gly	Thr
	210					215					220				
Ile	Asn	Tyr	Asp	Gln	Asp	Val	Asn	Gly	Ile	Met	Val	Gly	Val	Asp	Thr
225					230					235					240
Lys	Ile	Asp	Gly	Asn	Asn	Ala	Lys	Trp	Ile	Val	Gly	Ala	Ala	Ala	Gly
				245					250					255	
Phe	Ala	Lys	Gly	Asp	Met	Asn	Asp	Arg	Ser	Gly	Gln	Val	Asp	Gln	Asp
			260					265					270		
Ser	Gln	Thr	Ala	Tyr	Ile	Tyr	Ser	Ser	Ala	His	Phe	Ala	Asn	Asn	Val
		275					280					285			
Phe	Val	Asp	Gly	Ser	Leu	Ser	Tyr	Ser	His	Phe	Asn	Asn	Asp	Leu	Ser
	290					295					300				
Ala	Thr	Met	Ser	Asn	Gly	Thr	Tyr	Val	Asp	Gly	Ser	Thr	Asn	Ser	Asp
305					310					315					320
Ala	Trp	Gly	Phe	Gly	Leu	Lys	Ala	Gly	Tyr	Asp	Phe	Lys	Leu	Gly	Asp
				325					330					335	
Ala	Gly	Tyr	Val	Thr	Pro	Tyr	Gly	Ser	Val	Ser	Gly	Leu	Phe	Gln	Ser
			340					345					350		
Gly	Asp	Asp	Tyr	Gln	Leu	Ser	Asn	Asp	Met	Lys	Val	Asp	Gly	Gln	Ser
		355					360					365			
Tyr	Asp	Ser	Met	Arg	Tyr	Glu	Leu	Gly	Val	Asp	Ala	Gly	Tyr	Thr	Phe
	370					375					380				
Thr	Tyr	Ser	Glu	Asp	Gln	Ala	Leu	Thr	Pro	Tyr	Phe	Lys	Leu	Ala	Tyr
385					390					395					400

Val Tyr Asp Asp Ser Asn Asn Asp Asn Asp Val Asn Gly Asp Ser Ile
405 410 415
Asp Asn Gly Thr Glu Gly Ser Ala Val Arg Val Gly Leu Gly Thr Gln
420 425 430
Phe Ser Phe Thr Lys Asn Phe Ser Ala Tyr Thr Asp Ala Asn Tyr Leu
435 440 445
Gly Gly Gly Asp Val Asp Gln Asp Trp Ser Ala Asn Val Gly Val Lys
450 455 460
Tyr Thr Trp
465

<210> 381
<211> 207
<212> PRT
<213> E. Coli

<400> 381
Met Pro Val Lys Asp Leu Thr Gly Ile Thr Ala Lys Asp Ala Gln Met
1 5 10 15
Leu Ser Val Val Lys Pro Leu Gln Glu Phe Gly Lys Leu Asp Lys Cys
20 25 30
Leu Ser Arg Tyr Gly Thr Arg Phe Glu Phe Asn Asn Glu Lys Gln Val
35 40 45
Ile Phe Ser Ser Asp Val Asn Asn Glu Asp Thr Phe Val Ile Leu Glu
50 55 60
Gly Val Ile Ser Leu Arg Arg Glu Glu Asn Val Leu Ile Gly Ile Thr
65 70 75 80
Gln Ala Pro Tyr Ile Met Gly Leu Ala Asp Gly Leu Met Lys Asn Asp
85 90 95
Ile Pro Tyr Lys Leu Ile Ser Glu Gly Asn Cys Thr Gly Tyr His Leu
100 105 110
Pro Ala Lys Gln Thr Ile Thr Leu Ile Gln Gln Asn Gln Leu Trp Arg
115 120 125
Asp Ala Phe Tyr Trp Leu Ala Trp Gln Asn Arg Ile Leu Glu Leu Arg
130 135 140
Asp Val Gln Leu Ile Gly His Asn Ser Tyr Glu Gln Ile Arg Ala Thr
145 150 155 160
Leu Leu Ser Met Ile Asp Trp Asn Glu Glu Leu Arg Ser Arg Ile Gly
165 170 175
Val Met Asn Tyr Ile His Gln Arg Thr Arg Ile Ser Arg Ser Val Val
180 185 190
Ala Glu Val Leu Ala Ala Leu Arg Lys Gly Gly Tyr Ile Glu Met Asn
195 200 205
Lys Gly Lys Leu Val Ala Ile Asn Arg Leu Pro Ser Glu Tyr
210 215 220

<210> 382
<211> 64
<212> PRT
<213> E. Coli

<400> 382
Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys
1 5 10 15

Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro
20 25 30
Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp
35 40 45
Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys
50 55 60
Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu
65 70 75 80
Lys Ala Val Leu

<210> 344
<211> 68
<212> PRT
<213> E. Coli

<400> 344
Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
1 5 10 15
Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
20 25 30
Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
35 40 45
Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala
50 55 60

<210> 345
<211> 136
<212> PRT
<213> E. Coli

<400> 345
Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
1 5 10 15
Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
20 25 30
Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
35 40 45
Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
50 55 60
Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val
65 70 75 80
Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile
85 90 95
Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu
100 105 110
Ala Arg Glu Ala Phe Lys Leu Ala Ala Ala Lys Leu Pro Ile Lys Thr
115 120 125
Thr Phe Val Thr Lys Thr Val Met
130 135

<210> 346
<211> 123
<212> PRT

<213> E. Coli

<100> 386

Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
1 5 10 15
Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
20 25 30
Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
35 40 45
Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
50 55 60
Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
65 70 75 80
Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
85 90 95
Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp
100 105 110
Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
115 120 125
Met Pro Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
130 135 140
Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
145 150 155 160
Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
165 170 175
Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
180 185 190
Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
195 200 205
Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
210 215 220
Lys Lys Gln Gln Arg Lys Gly Arg Lys
225 230

<210> 3-7

<211> 111

<212> PRT

<213> E. Coli

<400> 3-7

Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys
1 5 10 15
Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala
20 25 30
Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys
35 40 45
Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala
50 55 60
Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro
65 70 75 80
Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile
85 90 95
Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg
100 105 110

<210> 288
<211> 2
<212> PRT
<213> E. Coli

<400> 288
Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu
1 5 10 15
Met Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg
20 25 30
Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr
35 40 45
Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp
50 55 60
Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr
65 70 75 80
Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys Lys
85 90

<210> 289
<211> 73
<212> PRT
<213> E. Coli

<400> 289
Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val
1 5 10 15
Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro
20 25 30
Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg
35 40 45
Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile
50 55 60
Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg
65 70 75 80
Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr
85 90 95
Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala
100 105 110
Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn
115 120 125
Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val
130 135 140
Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr
145 150 155 160
Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu
165 170 175
Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu
180 185 190
Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala
195 200 205
Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala
210 215 220

Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Arg Asn Phe
225 230 235 240
Gly Lys His Pro Val Thr Pro Trp Gly Val Gln Thr Lys Gly Lys Lys
245 250 255
Thr Arg Ser Asn Lys Arg Thr Asp Lys Phe Ile Val Arg Arg Arg Ser
260 265 270
Lys

<210> 39
<211> 169
<212> PRT
<213> E. Coli

<400> 39
Met Ile Asn His Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val
1 5 10 15
Ser Glu Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu
20 25 30
Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Ala Val Gln
35 40 45
Lys Leu Phe His Val Glu Val Glu Val Val Asn Thr Leu Val Val Lys
50 55 60
Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp
65 70 75 80
Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val
85 90 95
Gly Gly Ala Glu
100

<210> 40
<211> 271
<212> PRT
<213> E. Coli

<400> 40
Met Gln Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu
1 5 10 15
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val
20 25 30
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr
35 40 45
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly
50 55 60
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser
65 70 75 80
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val
85 90 95
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu
100 105 110
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala
115 120 125
Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu

```
    130                 135                 140
Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala
145                 150                 155                 160
Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp
                165                 170                 175
Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
            180                 185                 190
Val Lys Gln Val Glu Glu Met Leu Ala
        195                 200
```


(210) 392
(211) 209
(212) PRT
(213) E. Coli

(400) 392


```
Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
 1               5                  10                  15
Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
            20                  25                  30
Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
        35                  40                  45
Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
    50                  55                  60
Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
65                  70                  75                  80
Glu Phe Arg Leu Ala Glu Gly Thr Glu Phe Thr Val Gly Gln Ser Ile
                85                  90                  95
Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
            100                 105                 110
Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
        115                 120                 125
Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly
    130                 135                 140
Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys
145                 150                 155                 160
Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp
                165                 170                 175
Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala
            180                 185                 190
Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys
        195                 200                 205
Ala
```


(210) 393
(211) 103
(212) PRT
(213) E. Coli

(400) 393


```
Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
 1               5                  10                  15
```

Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
20 25 30
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
35 40 45
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
50 55 60
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
65 70 75 80
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
85 90 95
Asp Val Gln Ile Ser Leu Gly
100

<200> 44
<211> 118
<212> PRT
<213> E. Coli

<400> 44
Met Ala Arg Val Lys Arg Gly Val Ile Ala Arg Ala Arg His Lys Lys
1 5 10 15
Ile Leu Lys Gln Ala Lys Gly Tyr Tyr Gly Ala Arg Ser Arg Val Tyr
20 25 30
Arg Val Ala Phe Gln Ala Val Ile Lys Ala Gly Gln Tyr Ala Tyr Arg
35 40 45
Asp Arg Arg Gln Arg Lys Arg Gln Phe Arg Gln Leu Trp Ile Ala Arg
50 55 60
Ile Asn Ala Ala Ala Arg Gln Asn Gly Ile Ser Tyr Ser Lys Phe Ile
65 70 75 80
Asn Gly Leu Lys Lys Ala Ser Val Glu Ile Asp Arg Lys Ile Leu Ala
85 90 95
Asp Ile Ala Val Phe Asp Lys Val Ala Phe Thr Ala Leu Val Glu Lys
100 105 110
Ala Lys Ala Ala Leu Ala
115

<210> 45
<211> 71
<212> PRT
<213> E. Coli

<400> 45
Met Pro Lys Ile Lys Thr Val Arg Gly Ala Ala Lys Arg Phe Lys Lys
1 5 10 15
Thr Gly Lys Gly Gly Phe Lys His Lys His Ala Asn Leu Arg His Ile
20 25 30
Leu Thr Lys Lys Ala Thr Lys Arg Lys Arg His Leu Arg Pro Lys Ala
35 40 45
Met Val Ser Lys Gly Asp Leu Gly Leu Val Ile Ala Cys Leu Pro Tyr
50 55 60
Ala
65

<210> 396
<211> 180
<212> PRT
<213> E. Coli

<400> 396

Met Lys Gly Gly Lys Arg Val Gln Thr Ala Arg Pro Asn Arg Ile Asn
1 5 10 15
Gly Gln Ile Arg Ala Gln Glu Val Arg Leu Thr Gly Leu Glu Gly Glu
20 25 30
Gln Leu Gly Ile Val Ser Leu Arg Glu Ala Leu Glu Lys Ala Glu Glu
35 40 45
Ala Gly Val Asp Leu Val Glu Ile Ser Pro Asn Ala Glu Pro Pro Val
50 55 60
Cys Arg Ile Met Asp Tyr Gly Lys Phe Leu Tyr Glu Lys Ser Lys Ser
65 70 75 80
Ser Lys Glu Gln Lys Lys Lys Gln Lys Val Ile Gln Val Lys Glu Ile
85 90 95
Lys Phe Arg Pro Gly Thr Asp Glu Gly Asp Tyr Gln Val Lys Leu Arg
100 105 110
Ser Leu Ile Arg Phe Leu Glu Glu Gly Asp Lys Ala Lys Ile Thr Leu
115 120 125
Arg Phe Arg Gly Arg Glu Met Ala His Gln Gln Ile Gly Met Glu Val
130 135 140
Leu Asn Arg Val Lys Asp Asp Leu Gln Glu Leu Ala Val Val Glu Ser
145 150 155 160
Phe Pro Thr Lys Ile Glu Gly Arg Gln Met Ile Met Val Leu Ala Pro
165 170 175
Lys Lys Lys Gln
180

<210> 397
<211> 641
<212> PRT
<213> E. Coli

<400> 397

Met Pro Val Ile Thr Leu Pro Asp Gly Ser Gln Arg His Tyr Asp His
1 5 10 15
Ala Val Ser Pro Met Asp Val Ala Leu Asp Ile Gly Pro Gly Leu Ala
20 25 30
Lys Ala Cys Ile Ala Gly Arg Val Asn Gly Glu Leu Val Asp Ala Cys
35 40 45
Asp Leu Ile Glu Asn Asp Ala Gln Leu Ser Ile Ile Thr Ala Lys Asp
50 55 60
Glu Glu Gly Leu Glu Ile Ile Arg His Ser Cys Ala His Leu Leu Gly
65 70 75 80
His Ala Ile Lys Gln Leu Trp Pro His Thr Lys Met Ala Ile Gly Pro
85 90 95
Val Ile Asp Asn Gly Phe Tyr Tyr Asp Val Asp Leu Asp Arg Thr Leu
100 105 110
Thr Gln Glu Asp Val Glu Ala Leu Glu Lys Arg Met His Glu Leu Ala
115 120 125
Glu Lys Asn Tyr Asp Val Ile Lys Lys Lys Val Ser Trp His Glu Ala

130 135 140

Arg Glu Thr Phe Ala Asn Arg Gly Glu Ser Tyr Lys Val Ser Ile Leu
145 150 155 160

Asp Glu Asn Ile Ala His Asp Asp Lys Pro Gly Leu Tyr Phe His Glu
165 170 175

Glu Tyr Val Asp Met Cys Arg Gly Pro His Val Pro Asn Met Arg Phe
180 185 190

Cys His His Phe Lys Leu Met Lys Thr Ala Gly Ala Tyr Trp Arg Gly
195 200 205

Asp Ser Asn Asn Lys Met Leu Gln Arg Ile Tyr Gly Thr Ala Trp Ala
210 215 220

Asp Lys Lys Ala Leu Asn Ala Tyr Leu Gln Arg Leu Glu Glu Ala Ala
225 230 235 240

Lys Arg Asp His Arg Lys Ile Gly Lys Gln Leu Asp Leu Tyr His Met
245 250 255

Gln Glu Glu Ala Pro Gly Met Val Phe Trp His Asn Asp Gly Trp Thr
260 265 270

Ile Phe Arg Glu Leu Glu Val Phe Val Arg Ser Lys Leu Lys Glu Tyr
275 280 285

Gln Tyr Gln Glu Val Lys Gly Pro Phe Met Met Asp Arg Val Leu Trp
290 295 300

Glu Lys Thr Gly His Trp Asp Asn Tyr Lys Asp Ala Met Phe Thr Thr
305 310 315 320

Ser Ser Glu Asn Arg Glu Tyr Cys Ile Lys Pro Met Asn Cys Pro Gly
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His Val Gln Ile Phe Asn Gln Gly Leu Lys Ser Tyr Arg Asp Leu Pro
340 345 350

Leu Arg Met Ala Glu Phe Gly Ser Cys His Arg Asn Glu Pro Ser Gly
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Ser Leu His Gly Leu Met Arg Val Arg Gly Phe Thr Gln Asp Asp Ala
370 375 380

His Ile Phe Cys Thr Glu Glu Gln Ile Arg Asp Glu Val Asn Gly Cys
385 390 395 400

Ile Arg Leu Val Tyr Asp Met Tyr Ser Thr Phe Gly Phe Glu Lys Ile
405 410 415

Val Val Lys Leu Ser Thr Arg Pro Glu Lys Arg Ile Gly Ser Asp Glu
420 425 430

Met Trp Asp Arg Ala Glu Ala Asp Leu Ala Val Ala Leu Glu Glu Asn
435 440 445

Asn Ile Pro Phe Glu Tyr Gln Leu Gly Glu Gly Ala Phe Tyr Gly Pro
450 455 460

Lys Ile Glu Phe Thr Leu Tyr Asp Cys Leu Asp Arg Ala Trp Gln Cys
465 470 475 480

Gly Thr Val Gln Leu Asp Phe Ser Leu Pro Ser Arg Leu Ser Ala Ser
485 490 495

Tyr Val Gly Glu Asp Asn Glu Arg Lys Val Pro Val Met Ile His Arg
500 505 510

Ala Ile Leu Gly Ser Met Glu Arg Phe Ile Gly Ile Leu Thr Glu Glu
515 520 525

Phe Ala Gly Phe Phe Pro Thr Trp Leu Ala Pro Val Gln Val Val Ile
530 535 540

Met Asn Ile Thr Asp Ser Gln Ser Glu Tyr Val Asn Glu Leu Thr Gln
545 550 555 560

Lys Leu Ser Asn Ala Gly Ile Arg Val Lys Ala Asp Leu Arg Asn Glu
565 570 575

Lys Ile Gly Phe Lys Ile Arg Glu His Thr Leu Arg Arg Val Pro Tyr
580 585 590

Met Leu Val Cys Gly Asp Lys Glu Val Glu Ser Gly Lys Val Ala Val
595 600 605
Arg Thr Arg Arg Gly Lys Asp Leu Gly Ser Met Asp Val Asn Glu Val
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Glu Glu

<213> Homo sapiens
<211> 453
<212> PRT
<213> E. Coli

<400> 95
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35 40 45
Pro Lys Lys Val Met Trp His Ala Ala Gln Ile Arg Glu Ala Ile His
50 55 60
Met Tyr Gly Pro Asp Tyr Gly Phe Asp Thr Thr Ile Asn Lys Phe Asn
65 70 75 80
Trp Gln Thr Leu Ile Ala Ser Arg Thr Ala Tyr Ile Asp Arg Ile His
85 90 95
Thr Ser Tyr Glu Asn Val Leu Gly Lys Asn Asn Val Asp Val Ile Lys
100 105 110
Gly Phe Ala Arg Phe Val Asp Ala Lys Thr Leu Glu Val Asn Gly Glu
115 120 125
Thr Ile Thr Ala Asp His Ile Leu Ile Ala Thr Gly Gly Arg Pro Ser
130 135 140
His Pro Asp Ile Pro Gly Val Glu Tyr Gly Ile Asp Ser Asp Gly Phe
145 150 155 160
Phe Ala Leu Pro Ala Leu Pro Glu Arg Val Ala Val Val Gly Ala Gly
165 170 175
Tyr Ile Ala Val Glu Leu Ala Gly Val Ile Asn Gly Leu Gly Ala Lys
180 185 190
Thr His Leu Phe Val Arg Lys His Ala Pro Leu Arg Ser Phe Asp Pro
195 200 205
Met Ile Ser Glu Thr Leu Val Glu Val Met Asn Ala Glu Gly Pro Gln
210 215 220
Leu His Thr Asn Ala Ile Pro Lys Ala Val Val Lys Asn Thr Asp Gly
225 230 235 240
Ser Leu Thr Leu Glu Leu Glu Asp Gly Arg Ser Glu Thr Val Asp Cys
245 250 255
Leu Ile Trp Ala Ile Gly Arg Glu Pro Ala Asn Asp Asn Ile Asn Leu
260 265 270
Glu Ala Ala Gly Val Lys Thr Asn Glu Lys Gly Tyr Ile Val Val Asp
275 280 285
Lys Tyr Gln Asn Thr Asn Ile Glu Gly Ile Tyr Ala Val Gly Asp Asn
290 295 300
Thr Gly Ala Val Glu Leu Thr Pro Val Ala Val Ala Ala Gly Arg Arg
305 310 315 320
Leu Ser Glu Arg Leu Phe Asn Asn Lys Pro Asp Glu His Leu Asp Tyr

325 330 335

Ser Asn Ile Pro Thr Val Val Phe Ser His Pro Pro Ile Gly Thr Val
340 345 350

Gly Leu Thr Glu Pro Gln Ala Arg Glu Gln Tyr Gly Asp Asp Gln Val
355 360 365

Lys Val Tyr Lys Ser Ser Phe Thr Ala Met Tyr Thr Ala Val Thr Thr
370 375 380

His Arg Gln Pro Cys Arg Met Lys Leu Val Cys Val Gly Ser Glu Glu
385 390 395 400

Lys Ile Val Gly Ile His Gly Ile Gly Phe Gly Met Asp Glu Met Leu
405 410 415

Gln Gly Phe Ala Val Ala Leu Lys Met Gly Ala Thr Lys Lys Asp Phe
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Asp Asn Thr Val Ala Ile His Pro Thr Ala Ala Glu Glu Phe Val Thr
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Met Arg
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<210> 399
<211> 2994
<212> RNA
<213> E. Coli

<400> 399

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aacucaucuc ggggcaaguu ucguccuuag augcuuucag cacuuaucuc uuccgcauuu   180
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acugucucac gacguucuaa acccagcucg cguaccacuu uaaauggcga acagccauac   360
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aacuaccuac cagacacugu ccgcaacccg gauuacgggu caacguuaga acaucaaaca   720
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gccuucucac gaaguuaagg caccauuuug ccuagauccu ucacccgagu ucucucaagc  1260
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<212> RNA
<213> E. Coli

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<210> 411
<211> 76
<212> RNA
<213> E. Coli

<400> 411
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ccccuauugg acgcca 76

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<211> 1549
<212> RNA
<213> E. Coli

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ugucugggaa gcugccugau ggagggggau aacuacugga aacgguagcu aauaccgcau 180
aaugucgcaa gaccaaagag ggggaccuuc gggccucuug ccaucggaug ugcccagaug 240
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ggaauauugc acaaugggcg caagccugau gcagccaugc cgcguguaug aagaaggccu 420
ucggguugua aaguacuuuc agcggggagg aagggaguaa aguuaauacc uuugcucauu 480

gacguuaccc gcagaagaag caccggcuaa cuccgugcca gcagccgcgg uaauacggag 540
ggugcaagcg uuaaucggaa uuacugggcg uaaagcgcac gcaggcgguu ugguuaaguc 600
agaugugaaa ucccegggcu caaccuggga acugcaucug auacuggcaa gcuugagucu 660
cguagagggg gguagaauuc cagguguagc ggugaaaugc guagagaucu ggaggaauac 720
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<223> Primer Oligonucleotide

<400> 403
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<210> 404
<211> 18
<212> DNA
<213> Artificial
<220>
<223> Primer Oligonucleotide

<400> 404
acaatttcac acagcctc 18

<210> 405
<211> 159
<212> DNA
<213> Escherichia coli

<400> 405
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atcaccagca gatgaaataa cgataaccag aacaacgcct tatagcgttg agtttgcgag 120
aaaacgttca tattgtacct ttttgattaa ccattgggg 159

<210> 406
<211> 640
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(640)
<223> n = A,T,C or G

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ataaggggac aaagngaagg aagtggntat taanggannc gccaatgcga nttagggcag 180
accattcggc cattcgcctt cttggttatc gaagttcatc cagatagccg ttgccngacc 240
cacnagattc gcttcnggca caaagcccca gtaacggctg tccgcgctgt tgtcgcggtt 300
gtccgccatc atgaagtatt gtcccggagg aacaatccag gttgccagtt gttgccctgg 360
ctgctggtaa tacatcccca cctgatcctg cgcaatcggc actgtcagaa tgcggtgcgt 420
cacatcaccc agtgtctctt tacgctcgga aagacgaatt ccattttctt tggtttcgtt 480
tttcagcact tcaaagaatc cgctggtcgc ttccccacca ttacggcgtg agaaggtctg 540
aacaaaatcg ctcggttcca cgtttgagta ggtgaccggc agcgcgtttt cacacgcctg 600
gcccgaactg catcccggtt gaatcgtcag cctctttgag 640

<210> 407
<211> 682
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(682)
<223> n = A,T,C or G

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gacgtaagcg gatggagtgg ccggaaacct catagtgacc gcccaccagt tggcctgcat 180
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tggcaaaagt tgatgttttt tagtctgttg tcaaagccgc nattataccn gtaaccggca 480
ctacagcaca cgtagaaagc acccgacaat actcctggca tgggcgttaa agctcacagg 540
atgcngatct tttcttcact ggcctaaaaa gctgatattc tgtaaagagt tacacngtaa 600
cattcagatc gctatgaaat atcaacaact tggaaatctt tgnaaagcng gttggaaaat 660
ccaaagtatc tggttaagaa gc 682

<210> 408
<211> 309
<212> DNA
<213> Escherichia coli

<400> 408
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gttgctaatt caggattgtc caaaactcta cgagtttagt ttgacattta agttaaaacg 120
tttgccctta cttaacggag aaccattaag ccttaggacg cttcacgcca tacttggaac 180
gagcctgctt acggtcttta acgccggagc agtcaagcgc accacgtacg gtgtggtaac 240
gaacccccgg gaggtcttta acacgaccgc cacggatcag gatcacggag tgctcctgca 300
ggcaagctt 309

<210> 409
<211> 1167

<212> DNA
<213> Escherichia coli

<400> 409
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cagaacggac gtcctgtcgc agtatattaa gtcgtcgata gaaacaagca ttgaaaggca 180
cagcagtagt caaacagtgt gaaacgctac tggcgcctta cagcgcaaaa aggctggtga 240
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ttaacttcaa cttcagcgcc agcttcttcc agagcttttt tcagtgcttc tgcgtcgtct 360
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agaaccatgc cagttgcgcc acgtactgct ttgataacag caactttgtt agcgccagca 480
gcttccagaa ttacgtcgaa ttcagttttt tcttcagcag cttcaaccgg gccagcagct 540
acaacctcag cagcagcagc ggaaacaccg aatttttctt ycattgcaga gatcaagttc 600
tacaacgtcc attacagaca tagctgcaac tgcttcaatg awttgatctt tagtgataga 660
catttaaatk gttcctgaat atcagaataa gtttatacgt aagcgaatgc gttaaaaaga 720
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gccagcttcg cgacctgctt tacgcagttc agtcatttta tctacagtta cgcccacggg 1140
aatccgcaac tactgcaagc caagctt 1167

<210> 410
<211> 404
<212> DNA
<213> Escherichia coli

<400> 410
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tcgatagaaa caagcattga aaggcacagc agtagtcaaa cagtgtgaaa cgctactggc 180
gccttacagc gcaaaaaggc tggtgactaa aaagtcacca gccatcagcc tgatttctca 240
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<210> 411
<211> 162
<212> DNA
<213> Escherichia coli

<400> 411
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gtgcagattc taccaggtct ttagcttctt tcagacccag gccagttgcg ccacgtactg 120
ctttgataac agcaactttg ttagcgccag ca 162

<210> 412
<211> 825
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(825)

<223> n = A,T,C or G

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cgtctttgct cacgcctctt ttcagagcag ccgggtgcag attctaccag gtctttagct 420
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taaaaagata actgcgatta agcagctcct ttcgcatcgc gtacagcagc cagaggtcga 780
aacagtttgc cagccgaagg ttggcttttc agcctnnncn natta 825

<210> 413
<211> 425
<212> DNA
<213> Escherichia coli

<400> 413
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aacttcaact tcagcgccag cttcttccag agcttttttc agtgcttctg cgtcgtcttt 180
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tttcagaatt acgtcgaatt cagttttttc ttcagcagct tcaacccggc cagcagctac 360
atccacagca gcagcagcgg aaacacccga atttttcttc cattgcagag atcaagttct 420
caaac 425

<210> 414
<211> 126
<212> DNA
<213> Escherichia coli

<400> 414
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gcagattcta ccaggtcttt agcttctttc agacccaggc cagttgcgcc acgtactgct 120
ttgata 126

<210> 415
<211> 264
<212> DNA
<213> Escherichia coli

<400> 415
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attctaccag gtctttagct tctttcagac ccaggccagt tgcgccacgt actgctttga 180
taacagcaac tttgttagcg ccagcagctt tcagaattac gtcgaattca gttttttctt 240
cagcagcttc aacccggcca gcag 264

<210> 416
<211> 201

<212> DNA
<213> Escherichia coli

<400> 416
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ggaagttcag gcgctttgga tttcgcaacg tcagccatta cgcgcagcgc gtactgcagc 180
ggaccgtcga tcatcaggtc a 201

<210> 417
<211> 338
<212> DNA
<213> Escherichia coli

<400> 417
aattcagcag ttgacagtgg cataaacgta actggtgact tttgcccggc atgacgccgg 60
gctttttta ttattccgtg acttccagcg tagtgaaggc aaacttctcg ccatcaaata 120
gcccctgact ggttagtttt agcgcgggga tcactggcag agaaagaaac gccatctgaa 180
taaaaggata atgggtaaac ggaccgcatt cacgggcggc ggctttcaag gcgtcaattt 240

<210> 418
<211> 338
<212> DNA
<213> Escherichia coli

<400> 418
ttcttttttt cgtcaacggt gtccagaatc attttattta cctcgggtac ttatgctgat 60
tttattatt atggggaagg tgttatttat gagtttcatt tatgcggtaa cgacaatgaa 120
ctcgtgaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt 180
aatattattt aaatattatt ttgagcatat gcacataagg ttg 223

<210> 419
<211> 338
<212> DNA
<213> Escherichia coli

<400> 419
ttcttttttt cgtcaacggt gtccagaatc attttattta cctcgggtac ttatgctgat 60
tttattatt atggggaagg tgttatttat gagtttcatt tatgcggtaa cgacaatgaa 120
ctcgtgaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt 180
aatattattt aaatattatt ttgagcatat gcacataagg ttg 223

<210> 420
<211> 212
<212> DNA
<213> Escherichia coli

<400> 420
aatacgcggt atgcacgcct ttctttttct cgtcaacggt gtccagaatc attttattta 60
cctcgggtac ttatgctgat ttttattatt atggggaagg tgttatttat gagtttcatt 120
tatgcggtaa cgacaatgaa ctcgggaatt agtataagca gcgcgagaat aataatcatt 180
gtgcaaatgc taatttaatt aatactattt aa 212

<210> 421
<211> 338
<212> DNA
<213> Escherichia coli

<400> 421
ccctgtaaat tatcgcccgt ggcataaaaa ctgcgtccaa acgccgtctt tgccagcagc 60
caggccataa atgccaccag aattatcgtc aaccaaccaa ttgctgaaac gccaagcagc 120
agcgcggcgg agagctgttt cagttcggcg ggtaacccct caatccattt gccgccagtc 180
cacaccaaca tgatgccctc gtacaaccct aacgtgccaa gggtggcaac aatggcaggg 240
atccttagcc acgcgaccag gacaccgttg aaaaatcccg cgagcaaacc aagcagtaaa 300
gtcgcgacac aagcaacagg tagtgaatat cctgcgttca gtaacatccc caacagcacc 360
gcgcacattc cgggtaatcg aaccccactt gaaacatcaa tattgsgsgt aagcattwcc 420
aagcgttcgs gcccatkg 438

<210> 422
<211> 682
<212> DNA
<213> Escherichia coli

<400> 422
aattccccgg gatccgtcga ccgtgcgctt ccggttgtgg caacccgcga aatggcgcgg 60
cagtaagtat ggcggggtta ttccttcccc gttgaggaca ccgggttgtc aggttgacca 120
tacgcttaag tgacaacccc gctgcaacgc cctctgttat caattttctg gtgacgtttg 180
gcggtatcag ttttactccg tgactgctct gccgcccttt ttaaagtgaa ttttgtgatg 240
tggtcaatcc ggctgagcgc acgcggaaca gttaaaacca aaaacagtgt tatgggtgga 300
ttctctgtat ccggcgttaa ttgttaactg gttaacgtca cctggaggca ccaggcactg 360
catcacacca ttcattgttg aggacgcgat aatgaaaacg ttattaccaa acgttaatac 420
gtcctaaact tgttttgaaa ttggtgtcac tatcagtaac ccagtattta ctgaagatgc 480
cattaacaag agaaaacaag aacgggagct attaaataaa atatgcattg tttcaatgct 540
ggcttgttta cgtctgatgc caaaaggatg tgcacaatga attcagcatt tgtgcttgtt 600
ctgacagttt ttctgtttc cggagagcca gttgatattg cagtcagtgt tcacaggaca 660
atgcaggaat gatgactgca gc 682

<210> 423
<211> 600
<212> DNA
<213> Escherichia coli

<400> 423
gcggatccaa ttgtgactgc tctgccgccc tttttaaagt gaattttgtg atgtggtgaa 60
tggcgctgag cgcacgcgga acagttaaaa ccaaaaacag tgttatgggt ggattctctg 120
tatccggcgt taattgttaa ctggttaacg tcacctggag gcaccaggca ctgcatcaca 180
ccattcattg ttgaggacgc gataatgaaa acgttattac caaacgttaa tacgtctgaa 240
ggttgttttg aaattggtgt cactatcagt aacccagtat ttactgaaga tgccattaac 300
aagaaaaaac aagaacggga gctattaaat aaaatatgca ttgtttcaat gctggctcgt 360
ttacgtctga tgccaaaagg atgtgcacaa tgaattcagc atttgtgctt gttctgacag 420
tttttctgtt ttccggagag ccagttgata ttgcagtcag tgttcacagg acaatgcagg 480
aatgatgatc tgcagcaacc gaacagaaaa ttcccggtaa ctgttacccg gtcgataaag 540
ttattcatca ggataatatc gaaatcccgg caggtcttta aacagttccg taataaataa 600

<210> 424
<211> 100
<212> DNA
<213> Escherichia coli

<400> 424
gcgatccaac aagaagatgc ggttgtaccg tcatcacgca gatgcgcaaa gctactcagc 60
aactgaccct tcttcgcaat aagcacgcca ttagcgtcat 100

<210> 425

<211> 465
<212> DNA
<213> Escherichia coli

<400> 425
tcgcgtgttt accttcaaca tcggtaactt tctggcggat agtttcacgg taagcaacct 60
gcggtttacc tacgttcgct tcaacgttga attcacgctt catacggtca acgatgatgt 120
cgaggtgcag ttcgcccata cccgcgatga tggtctggtt agattcttcg tcagtccata 180
cacgaaaaca cgggtcttct ttagccagac ggcccagagc cagacccatt ttttcctggt 240
cagctttgat tttcggttca actgcgatgg agattaccgg ctcagggaat tccatacgtt 300
ccagaatgat cggcgcatcc gggtcacaca gggtgtcacc agtggttacg tctttcagac 360
cgatagcagc agcgatgtcg cccgcgcgaa cttctttgat ctcttcacgt ttgttagcgt 420
gcatctgaac gatacgaccg aaacgctcac gtgcagcttt cacgg 465

<210> 426
<211> 653
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(653)
<223> n = A,T,C or G

<400> 426
tgatcggctc aagcagaact ggtttcgctt tcttaaagcc ttctttaaag gcgatagaag 60
cagccagttt aaacgccagt tcagaggagt caacgtcatg gtaagaaccg aagtgcagac 120
gaatacccat gtctactacc gggtagcctg ccagcggacc tgctttcagc tgttcctgga 180
tacctttatc aacggccggg atgtattcgc cagggattac accaccttta atgtcgttga 240
tgaactcgta gcctttcggg tttgaacccg gctccagcgg gtacatgtcg ataacaacat 300
gacctacttg accacgacca ccagactgtt tcgcgtgttt accttcaaca tcggtaactt 360
tctggcggat agtttcacgg taagcaacct gcggtttacc tacgttcgct tcaacgttga 420
attcacgctt catacggtca acgatgatgt cgaggtgcag ttcgccatac ccgcgatgat 480
ggtctggtag attcttcgtc agtccataca cggnaagacg ggtcttnttt agccagacgg 540
gcccagagca gacccatttt tttctggcag ctttggnttc ggtcaactgc gatggaaata 600
ccaggctcaa ggaattcata cgtttcanaa tgatcggggc attccgggtc aca 653

<210> 427
<211> 268
<212> DNA
<213> Escherichia coli

<400> 427
cttccttaaa gccttcttta aaggcgatag aagcagccag tttaaacgcc agttcagagg 60
agtcaacgtc atggtaagaa ccgaagtgca gacgaatacc catgtctact accgggtagc 120
ctgccagcgg acctgctttc agctgttcct ggataccttt atcaacggcc gggatgtatt 180
cgccagggat tacaccacct ttaatgtcgt tgatgaactc gtagcctttc gggtttgaac 240
ccggctccag cgggtacatg tcgataac 268

<210> 428
<211> [illegible]
<212> DNA
<213> Escherichia coli

<400> 428
gtttgcggga gatgtaaggg ctaatctgaa tggctgcatt ccttgtttaa ggaaaaacga 60
atgactgatt gccgatacct gattaaacgg gtcatcaaaa tcatcattgc tgttttacag 120

ctgatccttc tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt 130
cggacgcacc tttaataact ataaataagt gtctgggcag atactatata aattaactta 240
gtgaatgatt atgctaatgt catcaattaa ataaatataa tggcgttaag gcttcccagt 300
aatataatta atactctact tccagagtag 330

<210> 429
<211> 465
<212> DNA
<213> Escherichia coli

<400> 429
gttttgggga gatgtaaggg ctaatctgaa tggctgcatt ccttgtttaa ggaaaaacga 60
atgactgatt gccgataccc gattaaacgg gtcatcaaaa tcatcattgc tgttttacag 120
ctgatccttc tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt 180
cggacgcacc tttaataact ataaataagt gtctgggcag atactatata aattaactta 240
gtgaatgatt atgctaatgt catcaattaa ataaatataa tggcgttaag gcttcccagt 300
aatataatta atactctact tccagagtag aatattaaat tttatccgcg tggtgcatca 360
gcactaattt atcccacaac tgttcttctg tctcgacatg cgccggatct ttcacaatag 420
tatttgggat cgggcacacc ttctggcagg ttggtgtctc gtagt 465

<210> 430
<211> 379
<212> DNA
<213> Escherichia coli

<400> 430
aatctgaatg gctgcattcc ttgtttaagg aaaaacgaat gactgattgc cgatacctga 60
ttaaacgggt catcaaaatc atcattgctg ttttacagct gatccttctg ttcttataac 120
acaaggaaac gtacttaagg tgcgtccggt gaaccagtcg gacgcacctt taataactat 180
aaataagtgt ctgggcagat actatataaa ttaacttagt gaatgattat gctaatgtca 240
tcaattaaat aaatataatg gcgttaaggc ttcccagtaa tataattaat actctacttc 300
cagagtagaa tattaaattt tatccgcgtg gtgcatcagc actaatttat cccacaactg 360
ttcttctgtc tcgacatgc 379

<210> 431
<211> 443
<212> DNA
<213> Escherichia coli

<400> 431
aagatgatgt gatgagaaag tcaatttgaa taagacaata ttaagagcta aaaaaatgtc 60
aaaaaatact aaatcaaaaa ataatggcat tagaaaatat aatgcgaaaa cggaggtgaa 120
atttatttat ttcaaatgag gaaaatctcc cggcgaaaaa acggggagat gaaagtgtga 180
tgggtatcaa ataaacaaca gaggagaaat ttttaacgca gccattcagg caaatcgttt 240
aatcacattg cctggcggat aagttgcggc ttaacgccag gaagcgtgtc ggccagtttc 300
aaacaaatat cacgcagcag ttttttcgcc ggattggtac cggaaaacag atcgcggaat 360
tcctgcatac cagccagcat caacgccgca ctgtgcttgc ggctacgctc atagcgacgc 420
agataaatgt actgcccgat gtc 443

<210> 432
<211> 673
<212> DNA
<213> Escherichia coli

<400> 432
caggggtttt gttgtgggca atgatgcatt taagttatcg tctgcagata gaggagatat 60
tacaataaac aacgaatcag ggcatttgat agtcaatacc gcaattctat caggagatat 120

agtcactcta agaggaggag aaattaggtt ggtattatag cttgtgcgcg ccatgattgg 120
cgcgcaattt aaacttagtg ctttacatcg ctattgtctt gatttctttg aattatttta 240
taaattaaaa aaacgactgt tatgtataag caaaggtccg aacgaaaaat acattccaaa 300
taaaatgcttg cttaaatctc tatatccttc ccgaaaaaat gacacataaa attgagatat 360
tccaaaaaga gatactacaa ataaagatgc ctttatttta ttatttctaa taaaaataga 420
agcaattaaa aataataaca atgatataaa tctaatgttt ttaaatatat tgtcttttat 480
gttagtaata gtcgttagta tgtttgattc tccatatatt acgtgtagtt ttttatatac 540
atggaaataa ttttcttta actgagacat cacaccatca tcaaatggaa gtttgaagat 600
ggtgcttggt ttgctaacca ataaaaagag tgcattcg 638

<210> 433
<211> 249
<212> DNA
<213> Escherichia coli

<400> 433
cttiacttgg catgatccac ttcgccagaa taccggcaat aagcccaaaa ataatccatg 60
acagaatgcc cattgtttcc tcacttatct gttttgcatt agcgggttag tcgctgataa 120
aaagcatagc acaacatcgg gagggcaaga tttgtgacga gcatcacgga ggttttttg 180
cgatggcgca gaaattgcgc catcaacgat cagtgataat taccaaccac aaacatcatg 240
ttcgtttttcc gtgtcataag aacgtacggt attcacgaga tcttttatca ctttagccg 299

<210> 434
<211> 399
<212> DNA
<213> Escherichia coli

<400> 434
aaaaaatgag gcaatatcgg gtaaaggcat cagccggacg aatacgtcgg gctacaaata 60
ttattgtcct gcaggtgttt tagcgggttg ttgatccaca ggttctaact ggaagaccac 120
acgaccttga tcatcaaact gaatagcggc ctgcctcgtaa gtttcctggg cggacacgg 180
gccttcatcg gctttcatca tccgcaccat tgggctgggc tgatagttgg aaacatggta 240
cggcacgtta tatacgggcc ccagtttacg atgaaagccg ttcgccagtt cctgcgcctg 300
atgaatcccg ttatcaatcg ctgccttacg cgctttgtct ttataggcat ccggctgcgc 360
aacgccagc gacacagaac gaattccc 388

<210> 435
<211> 501
<212> DNA
<213> Escherichia coli

<400> 435
ctatccttga tgaaaccgcg agcaaagata ggtgattacg tcatggtttt acagaaaatt 60
tcagaaaaag gaggcaatat cgggtaaagg cattagccgg acgaatacgt cgggctacaa 120
acattatgt gctgcaggtg ttttagcggg ttgttgatcc acaggttcta actggaagac 180
cacatcgacc tgatcatcaa actgaatagc ggcctgctcg taagtttcct gggcggacac 240
cggcacggca tcggcttttca tcatccgcac cattgggctg ggctgatagt tggaaacatg 300
gtacgcgacg ctatatacgg gccccagttt acgatgaaag ccgttcgcca g 351

<210> 436
<211> 762
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(762)

<223> n = A,T,C or G

<400> 436
aattatgaaa cactgtctgg aatcgtctga atgacgggca catttgcgag cacgcatcca 60
gtaataacac aggaaactat tttatctacg cgttagcgat agactgcttg catggcgaaa 120
ggaggtaagc cgacgatttc agcgggacgc tgaaacggga aagcccctcc cgaggaaggg 180
gccataaata aggaaagggt catgatgaag ctactcatca tcgtggtgct cttagtcata 240
agcttccccg cttactaaga ctaccagggc gggggaaacc ccgctctacc ctcactcctg 300
aagtatgcct ttcacgataa gattgtcaat ccgcaggctt tgtagtctgc gatcctgcca 360
gcaaatattc tttgcgagtc gttacgcaat aatcacagag gaaactattt tattcacgcg 420
ttagcgatag actgcattca gggcgaaagg aggtaagccg atgatttcag cgggacgctg 480
aaacgggaaa gcccctcccg gagaagaggg cttttaataa ggaaagggtt atgatgaagc 540
acgtcatcat actggtgata ctcttagtga ttagcttcca ggcttactaa gaacaccagg 600
gggaggggga aaccctttcc taaccctcac ttctgaaatt gggtgctatg acgctggcgt 660
tactgcttan cgctaccagt ttgtctgccc tggcggttgt aacgccagat cggtacccgt 720
ttggatattt taatgaaagc cgacaaatca atcancgtga cg 762

<210> 437
<211> 290
<212> DNA
<213> Escherichia coli

<400> 437
cacatttgcg agcacgcatc cagtaataac acaggaaact attttatcta cgcgttagcg 60
atagactgct tgcatggcga aaggaggtaa gccgacgatt tcagcgggac gctgaaacgg 120
gaaagcccct cccgaggaag ggccataaat aaggaaaggg tcatgatgaa gctactcatc 180
atcgtggtgc tcttagtcat aagcttcccc gcttactaag actaccaggg cgggggaaac 240
cccgctctac cctcactcct gaaagtatgc ctttcacgat aagattgtca at 290

<210> 438
<211> 631
<212> DNA
<213> Escherichia coli

<400> 438
atttacactt tttacgaaat catggatcca ctaacaaaat atcgcttgtc agttatattg 60
tatgccagca aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 120
ttaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tgggccgcac 180
cagccacgcc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 240
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 300
attcaaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 360
ggacctatat gggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 420
cctacgacgg tgagattttt tatcatcgct aaaaaagccc ccctcatcat gagggggaaa 480
tccacacacc ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtcg 540
tattccacgt tgattaatgc ggttgcctcc agtgcgccag atttaacttt gtttgtatcg 600
ttgacgtagt aactggctgt tatcggaatt g 631

<210> 439
<211> 566
<212> DNA
<213> Escherichia coli

<400> 439
tatgccagca aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 60
ttaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tgggccgcac 120
cagccacgcc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 180
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 240

agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 300
ggacctatat gggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 360
cctacgacgg tgagattttt tatcatcgct aaaaaaagcc cctcatcat gaggggaaaa 420
tgcagacacc ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtcg 480
tattttcacgt tgattaatgc ggttgccttc agtgcgccag atttaacttt gtttgtatcg 540
tagacgtagt aactggctgt atcgaa 566

<210> 440
<211> 339
<212> DNA
<213> Escherichia coli

<400> 440
gttattgaca tcctttttgat tggtgataac atgcgaatcg gtattatttt tccggttgta 60
atcttcatta cagcgggtcgt atttttagca tggttttttta ttggcggcta tgctgccccg 120
ttagcataaa gatgaaaaaa acaacgatta ctatgatggg tgtggcgatt attgtcgtac 180
tcggcaatga gctgggatgg tggtaacgtc acctctaaaa aatagcaaag gctgcctgtg 240
tgcagccttt gtgcaattta agcgtttaac tttaatcttc ctgtagataa atagcacgac 300
aatctcaaca ataacggcaa ccacgaagct gccaaaatt 339

<210> 441
<211> 576
<212> DNA
<213> Escherichia coli

<400> 441
tatgtattct taaaaaggaa aacgacatga aacgaagca cagaatcaac attctccaat 60
tatcaaatat ttccgtggag catttttatta ttgaatatag aggtttaact ccggtaaaaa 120
acaaagaatc attgaatgca gggaaaaata atatggccat aaaaaacatc gaaagaaact 180
cttttaattt aacatgtaaa cgcatggtta atcctcatat cacgggtgga gtgttaagaa 240
tatatatcaa tggagtcatg ttttcccttt tccatttatc aagttcctgt tgccgttttta 300
tccatttct aattgcatat tttaatttct ctgataaatg gcattgagca tcgatttcat 360
ttaaaacaac tgtaca 576

<210> 442
<211> 446
<212> DNA
<213> Escherichia coli

<400> 442
tcacgatagc tattagtaaa aatataagag ttagctgtat tgttatgtct gtgtgcgaaat 60
tcactacctt cgttttttttg attaagaatg attttattat cgtaagtaaa attcatgaa 120
tatttaaaaa ggaaaacgac atgaaacgga agcacagaat cacatttctc caatcataaa 180
ttatttcgct ggagcatttt attattgaat atagaggttt aactccggta aaaaacaaag 240
aagcattgaa tgcagggaaa aataatatgg ccataaaaaa catcgaaaga aactctttta 300
atttaacatg taaacgcatg gttaatcctc atatcacggg tggagtgtta agaacataca 360
taaatgcatt catgttttcc cttttccatt tatcaagttc ctgttgccgt tttagtccat 420
atctaattgc atattttaat ttttct 446

<210> 443
<211> 346
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(388)

<223> n = A,T,C or G

<400> 443
tcaccccggt gccgattttc aggcatcctg atttaactta gcacccgcaa cttaactaca 60
gaaaaacaaa gagataaatg tctaatcctg atgcaaatcg agccgatttt ttaatcttta 120
cggactttta cccgcctggt ttattaattg cactgtnatc cgggcgttcg cccgctttaa 180
tcataatagg ctgtgtagcc tgggcctgtt tctctttcac ccgcgccaga gcggcagcaa 240
tcgcatcttt atctttggct gcaggttgaa cggctgcgct cttatgtcgt tcaaggcgag 300
cccgcttttc gcgctccaga cgagcctggc gcgcttcgaa acgcgctttg gcttctgcgg 360
cncgcttttc ttcctgacga atagccgc 368

<210> 444
<211> 209
<212> DNA
<213> Escherichia coli

<400> 444
aattttaata acgctatctg cggataaagc agaataggtg gttaacccca gacataaacc 60
gagcaaaata atgttattgt atttcataat ctattgttcc ttagcgacag attgctgtct 120
gctcatttag taaggtacca ggagaaactt caggaagctt gtactcgaca atacagtttg 180
actttttatc tttgccccat gaaacctgt 209

<210> 445
<211> 341
<212> DNA
<213> Escherichia coli

<400> 445
catcattaat accgttaaat gcaacccgaa cccccgttgt ccctttgctg cattcactta 60
acgtaattcg aaaagggacg gctggacttg tgctaccggt cgttggaaat tgtctggcac 120
tgtttttttg gagatctacg gtaaaattaa gcgaatccga tgagactgtg cagccataat 180
cgacaatgcg cccgctaatt ttaataacgc tatctgcgga taaagcagaa taggtggtta 240
acccaagaca taaaccgagg aaaataatgt tattgtattt cataatctat tgttccttag 300
ctacagattg ctgtctgctg gttcagtaag gtaccaggag a 341

<210> 446
<211> 697
<212> DNA
<213> Escherichia coli

<400> 446
aaatttactg ccaatttccg gcagatcgga aagggttaam ccatattgat ccataagggt 60
acgaatcmcg ggctatacgg ccaggcatgg cttgagccat ggcattaaat tccgcaaatt 120
cgggcgctga ttcttcccac gcggttattt tggcacacac cagatccagc aaggggtttt 180
caggatcgtt gagcagcaga tgatctacca gttccagcgc ctgggtgtat tgttcctcgt 240
tctgaatacc cgccagaaaa ggtgccacag cagttagctt ttctcctgct tgcaagatgt 300
cggcaatcgc aatcattttt tccccttagt acgatgaaca gcggtaaaga aatcgtattc 360
tttatgcgtc ataacttcac gtatgtagca cttttgcgat tcaaaaaaga ccattgctac 420
aacaagtaat tcattgcccc caacattgaa aacataatgc ttatccagat atttgaagtt 480
atccagagat gggaatactg cttttaatga ctcaggtttt ttgaaatatc ccttagcaat 540
cgtgatcccc agagccacca actccgtttt atgttgcggg tatttttccg cagcatcttt 600
caatgctttt tgagttatca ggtgcattct tcatcacgtc cgtkgmcaaa ttggcaatat 660
gataacatcc gttgccagat tggcacggat gaattat 697

<210> 447
<211> [illegible]
<212> DNA

<213> Escherichia coli

<400> 447
aattaataac ttttcgttag gcagttttgg gtgtgagttg caagagggga gactactgaa 60
tgaactcaagt tttataatcg aggggaaaat ggtgatgggg ttcatagcaa aacgcctcca 120
gccataaagg tcgagggcgc ttaagatgtt aaaaaccggc tatccgttaa aaaacaatgt 180
tctaattaagg tcagtgacat tgcgctaaaa aagcg 215

<210> 448
<211> 345
<212> DNA
<213> Escherichia coli

<400> 448
gcattattca tgagaaatgt gtatcgtaaa tcaactgaaa ttaacgcaac catttgttat 60
ttaaatgttta attatctgtg tgtgatattt tattgaatgt tttaaatatt gttttattg 120
gcattgctat aatattggtt atcatttgct gaatggattc agtcttaatg agtgggtttt 180
tgaacggacag gcatagagta atgatacgta tgcataacca acatctttac tcattatgtc 240
attgaatgtt gacgctatgt gtttatgagg gagaggtatt ttcagttgat ctggattgtt 300
tcatttcatat aatgcgcctt tgctcatgaa tggatgccag tatgtagtgg gaaattataa 360
tcattgaaat agtccaacta cttcttttatt accaa 395

<210> 449
<211> 641
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(641)
<223> n = A,T,C or G

<400> 449
gtaaatcaggt aagaaaaggt gcgcggagat taccgtgtgt tgcgatatat tttttagttt 60
agcgtggcaa tacatcagtg gcaaataaaac gacatatcca gaaaaatata cactaagtga 120
atcatatctt ccgatttatc ttaatcgttt atggataacg gcaaagggct tcgttttttc 180
ttatacttat tcagcactca caaataaagg aacgccaatg aaaattatac tctgggctgt 240
attcattatt ttcctgattg ggctacttggt ggtgactggc gtatttaaga tgatatttta 300
aaatttaatta atgtcatcag gtccgaaaat aacgagaata tttcagtctc tcatcctgtt 360
gtgctcttgt catgtgcatt gcttcatata atcactgggg caaggagcgc cgcaggcgna 420
ncntncncgn cgncccacct nacccatgc cgaacttcag aantgaaaac ncnntaacnc 480
ctttngttcgg cgggngcctc cccatgcnan agtangggaa ntgccangcg ncnnattaaa 540
ccgaaaggcth attncaaaga ctgggccttn cntttatctg atgtttgtcg gagaacgctc 600
tcttcagcnan gacaaatncc gccgggagcg gatttgaacn t 641

<210> 450
<211> 314
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(314)
<223> n = A,T,C or G

<400> 450
gaactacgag taagaatagc tncgaattcc cgtttangga taacggcaaa gggcttcgtt 60

ttttcctata cttattcagc actcacaaat aaaggaacgc caatgaaaat tatactctgg 120
gctgtattga ttatttttct gattgggcta ctggtggtga ctggcgtatt taagatgata 180
ttttaaaatt aattaatgtc atcaggtccg aaaataacga gaatatttca gtctctcatc 240
ctgttgcgct cctgtcatgt gcattgcttc atataatcac tggcgcaagg agcgcgcagg 300
gggntntnnt cttt 314

<210> 451
<211> 336
<212> DNA
<213> Escherichia coli

<400> 451
atatncaata agtgaatgat atcttccgat ttatcttaat cgttttatgga taacggcaaa 60
gggcttcgtt ttttcctata cttattcagc actcacaaat aaaggaacgc caatgaaaat 120
tatactctgg gctgtattga ttatttttct gattgggcta ctggtggtga ctggcgtatt 180
taagatgata ttttaaaatt aattaatgtc atcaggtccg aaaataacga gaatat 236

<210> 452
<211> 414
<212> DNA
<213> Escherichia coli

<400> 452
ctgnnattac cgtgtgcttc gatatatttt ttagtttcgc gtggcaatac atcagtggca 60
atataacgac atatccagaa aaatatacac taagtgaatg atatcttccg atttatctta 120
atcgttatcg gataacggca aagggcttcg ttttttccta tacttattca gcactcacaa 180
atanagtaac gccaatgaaa attatacttc gggctgtatt gattatttcc ctgattgggc 240
tactctgtct gactggcgta tttaagatga tattttaaaa ttaattaatg tcatcaggtc 300
cgaannatac gagaatattt cagtcttcca tcctgttgcg ctccctgtcat gtgcattgct 360
tcaantaatc actgggcgcaa ggagcgcgca gggggcgggc aatcgccgcc gccccctg 419

<210> 453
<211> 351
<212> DNA
<213> Escherichia coli

<400> 453
aacaattttc ccatgcgctc ggtcatgcgc tgcatcgccc ggccatttta sgcgtcccag 60
cgannggcat tcgactgtta atgggcgaat cttcagtact ggtattaggt ggacaacgcg 120
cgctncctaa acggctggaa gaagcgggtt ttgcgtttcg ctggtacgat ttagaagagg 180
cgctcgcgga tgtcgttcgc tgatgtggtt tacagcaaac atccgccagt taactcccgg 240
ngttccagga ttagtggctt tgcgcgataa gatcgtctgg tgaaagtcgg gtcaccatca 300
taacraaatc tctgtctaaa cctctatcca gcattcctg agcaatacgc agggcttctt 351
<210> 454
<211> 96
<212> DNA
<213> Escherichia coli

<400> 454
tggcatctcg gtgttgccga tcttcatgat atccagcccg ccggaaactt cttcccaaac 60
ggttttgctg ttatccattg agtcacggaa ctg 93

<210> 455
<211> 232
<212> DNA
<213> Escherichia coli

<400> 455
[illegible] tgatcctgta accatcatca gttgtgaagt agtgattcac gacttcaagg 60
[illegible] aagggtattt tggctttgac atattagggg ctattccatt tcatcgtcca 120
[illegible] tgcagtacat actcgttgga aatcaacaca ggaggctggg aatgccgcag 180
[illegible] tactttcttt aatagtgatt tgtttcacgc ttttattttt ca 232

<210> 456
<211> 713
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(713)
<223> n = A,T,C or G

<400> 456
[illegible] naangcccac ancctcgang gatctaggag gtagaatagc ttcgaattcc 60
[illegible] gcggcctttct tcgtcagatt tcgcagtagt ggtaatggta atatccaaac 120
[illegible] gtcgacttta tcgtagtcga tttctgggaa gatgatctgc tcacggacac 180
[illegible] gttaccacga ccgtcgaaag acttagcgga caggccacgg aagtcacgga 240
[illegible] agcaatagtg atcaggcgct caaagaactc ccacatgcgt tcgccacgca 300
[illegible] acagccgatc ggatagccct gacggatttt gaagcctgca acagatttgc 360
[illegible] gatcagcggt ttttgaccgg agattgctgc caggtctgct gctgcgttat 420
[illegible] tttgtcagcg atcgctttcac caacacccat gttcagggtg atctttctcga 480
[illegible] ttgcatgaca gaattgtagt taaactcagt catgagtttt ttaactactt 540
[illegible] gtaatcatgc agtttcgcca tcgtactact ccatgtcggt gaacgctctc 600
[illegible] caaatccgcc ggagccggat ttaacgttgc gaacaaccgn cccggagggg 660
[illegible] accccgccat aactggcagc attaaattaa gcagaaggcc atc 713

<210> 457
<211> [illegible]
<212> DNA
<213> Escherichia coli

<400> 457
[illegible] agatacggcc agtgcggcca atgtttttg tcctttaaac ataacagagt 60
[illegible] tatagaatag gggtatagct acgccagaat atcgtatttg attattgcta 120
[illegible] ttgcttaaaa atattgttag ttttattaaa tgcaaaacta aattattggt 180
[illegible] tgttgtatga tgaataaaat ataggggggt atagatagac gtcattttca 240
[illegible] aatgcgacta ccatgaagtt tttaattgaa agtattgggt tg 292

<210> 458
<211> [illegible]
<212> DNA
<213> Escherichia coli

<400> 458
ttattaaatg caaaactaaa ttattggtat catgaatttg ttgtatgatg aataaaatat 60
aggggggtat agatagacgt cattttcata gggttataaa tgcgactacc atgaagtttt 120
taattgaaag tattgggttg ctgataattt gagctgttct attcttttta aatatctata 180
taggtctgtt aatggatttt atttttacaa tttttgtgt ttaggcatat aaaaatcaac 240

ccgccatatg aacggcgggt taaaatattt acaacttagc aa 282

<210> 459
<211> 300
<212> DNA
<213> Escherichia coli

<400> 459
tctgcgttcc gctaaaaggt gcaaatgctc aggacgttgc agcgttttgc gtgaccgctc 60
gggaaaggca aaattgcctc tgggaaagca ttgcgcgggg tccggcgctc atcaacaatc 120
gggggcaac aagggggctga aacgggaaag cccctcccga agaaggggcc ttgtataagg 180
aaaggttaat gatgaagctc gtcatcatac tggttgtgtt gttactgtta agtttcccga 240
cttactaaca actcatcaga gggggagaa atcctccctt accccttgttc ctttactcta 300

<210> 460
<211> 293
<212> DNA
<213> Escherichia coli

<400> 460
cgggctcggg cgctcatcaa caatcggggg gcagcaaggg gctgaaacgg gaaagcccct 60
ccctaaagaag gggccttgta taaggaaagg gttatgatga agctcgtcat catactggtt 120
atgttgttac tgttaagttt cccgacttac taacaactca tcagaggggg gagaaatcct 180
ccctacctct tgttccttta ctctaggttg aaaaaacaac agcgtcaata ggcctgccat 240
ttaataagtg agatctgtga acggctttcc ggttagcctt ttttatcctg ttg 293

<210> 461
<211> 359
<212> DNA
<213> Escherichia coli

<400> 461
caatacagga ggctgggaat gcggcagaaa tatagattac tttctttaat agtgatttgt 60
ttcatgcttt tatttttcac ctggatgata agagattcac tgtgtgaatt gcatattaaa 120
caggagaatt atgagctggc ggcgttttta gcctgcaaat tgaaagagta agagtcttcg 180
ccgcaaaatt atttcccgcct tacttacggc gttgcgcatt ctcattgcac ccaaatttat 240
tcttcacaaa aataataata gattttatta cgcgatcgat tatttatttc ctgaaaacaa 300
ataaaaaaat ccccgccaaa tggcagggat cttagattct gtgcttttaa gcagagatt 359

<210> 462
<211> 673
<212> DNA
<213> Escherichia coli

<400> 462
ccaaccatg tcctgacctg ggttcggggg acaccaaaac gtgccgagat gatcctgtaa 60
ccatcatcag ttgtgaagta gtgattcacg acttcaaggc gcttttcaaa agggtatttt 120
ggctttgaca tattaggggc tattccattt catcgtccaa caaaatgggt gcagtacata 180
ctcgttggaa atcaacacag gaggctggga atgccgcaga aatatagatt actttcttta 240
atagtgattt gtttcacgct tttatttttc acctggatga taagagattc actgtgtgaa 300
ttgcatatta aacaggagag ttatgagctg gcggcgtttt tagcctgcaa attgaaagag 360
taagagtctt cggcgggaaa ttatttcccgc cttacttacg gcgttgcgca ttctcattgc 420
acccaaattt attcttcaca aaaataataa tagattttat tacgcgatcg attatttatt 480
tcctgaaaac aaataaaaaa atccccgcca aatggcaggg atcttagatt ctgtgctttt 540
aagcagagaa tacaggctgg ttacgttacc agctgccggg cctttagcgc cgctttcgat 600
ggtgaaggac actttctgac cttcgtccag agatttgtaa ccatcgttct ggatagcaga 660
gaagtgtacg aac 673

<210> 463
<211> 630
<212> DNA
<213> Escherichia coli

<400> 463
tagtggcatt ggttgctgga gagagaaaac ccccgcacgt tgcaggtatg cacctgacaa 60
taccacgggg gctaatcttg actctagacc actcaagaat agccgcgaaa cgttgtcatt 120
acaacacagg cggctatatg acgttcgcag agctgggcat ggccttctgg catgatttag 180
cagctccggt cattgctggc attcttgcca gtatgatcgt gaactggctg aacaagcgga 240
agtaacgtgt catgcgggcg tcaggctgcc gtaatggcaa tttgcgcccg gaccaggccg 300
caggggggaa actctgcggc ctttttcgtt cttactgcgg gtaaggcacc cagtcgccgc 360
cgttcaggcg aacgtacggt ttatcctggt attgaataac tactgcattt gagttctcgg 420
agaccggtgc tgtttgtggc aacccactgg tgagtttttt ccagtcaaca ttgtcttcgg 480
tgaaaatctt gccatcgaga acgcgaacca ccagatcgga gatagccagg aagctgctcg 540
ctcgttcgat gacaatcggt gccccctgat gcggtgcctt catgccgaag aatttcaccc 600
caacgggcac gtcggtgata gacgggctag 630

<210> 464
<211> 391
<212> DNA
<213> Escherichia coli

<400> 464
ctcaggctgc tgattgtttt tttgtgcaat ggcgcggtat tagcgtcgtt gctgtcgatg 60
gagaaaatca taaacgtggt gaatgatgat tgttagcaag gaaaactgtc aaaaatcttc 120
caaaaatttg aggataaagg ccggaatggc tccggccaga gggaagttaa ccgcgaagct 180
gttgctgctt gagggtcgtt ttaaccagac gccaggcgct ccatacgcca aaaccgcgtc 240
tggcccacgg gaccagcata ttaggatggc gaatcgtcca gatcgccatc acgctactgc 300
caaccagtgc ccaggagcgc agacttagca gcatattcca gcgacgatcg taagcgcctg 360
ttgtctcaag ccattcacga cgactggcgg a 391

<210> 465
<211> 625
<212> DNA
<213> Escherichia coli

<400> 465
aacacaccac accataaacg gaggcaaata atgctgggta atatgaatgt tttaatggcc 60
gtactggaaa taattttatt ttctggtttt ctggccgcgt atttcagcca caaatgggat 120
gactaatgaa cggagataat ccctcaccta accggcccct tgttacagtt gtgtacaagg 180
ggcctgattt ttatgacggc gaaaaaaaac cgccagtaaa ccggcggtga atgcttgcat 240
ggatagattt gtgttttgct tttacgctaa caggcatttt cctgcactga taacgaatcg 300
ttgacacagt agcatcagtt ttctcaatga atgttaaacg gagcttaaac tcggttaatc 360
acatttttct cgtcaataaa catgcagcga tttcttccgg tttgcttacc ctcatacatt 420
gcccggttcg ctcttccaat gaccacatcc agaggctctt caggaaatgc gcgactcaca 480
cctcactgca cggtaatgtt gatatgccct tcagaatgtg tgatggcatg gttatcgact 540
aactggcaaa ttctgacacc tgcacgacat gcttcttcat cattagccgc tttgacaata 600
atgataaatt cttcgccccc gtagc 625

<210> 466
<211> 6[illegible]3
<212> DNA
<213> Escherichia coli

<400> 466

tgcttttgaa tatgtgctcg caatcttgag aaggaaatgg cgaccacgaa agaaaaggca 60
aaaacgataa tctgaaagag ccaaggtatt tcagtataag cattgaatgc gacagtaaac 120
tctttcggta tcagccagag agtgagacca aaaatgataa tcgtatacat aagtctttcg 180
agtggctcgt tagcaaaaag tttcaacaat ggagtaaata catccaacat atcaataact 240
ctcatctgta agggtattga aatgttaaca caagctctcg ctgtaggggt atagccgaga 300
caacagaagc ccggaggtgg tgaaataaaa ccgggcacaa cacgaaggcg catttccgat 360
atccataaag agtcggtctt gtctgttaaa tttaaatggt gggagtgcgc ctccggttgt 420
aaataacgac attgctgtgt gtagtcctgg cggcatcagt ttttttcttg aagttcggct 480
gatgtccgcc ccttttaaag tgaattttgt gatgcggtga atgcggctaa gcgcacgtgg 540
cacagcttaa agtcatgtta gtccttattg gtttgggtgg gaaagccgac tgtaattgtt 600
aactagttgc agtcacctgg agg 623

<210> 467
<211> 234
<212> DNA
<213> Escherichia coli

<400> 467
tatttacata caagagattc atctttgtat aaataaagat aagtaattac gcataaaaca 60
ataatgatta taatagcaaa aataaatatt atcatctttg atagattact tgagatagcc 120
atcatcttgt aaagccttta tcgttttttt atgctctgga ttaatataat cactacatct 180
atcttacaaa tctgttgttg atggacatgt caacccatgg tcatttacag ccaa 234

<210> 468
<211> 519
<212> DNA
<213> Escherichia coli

<400> 468
attaactatt tcggctaaaa tagagactac atgtcttcgg tccatctcac ttaaggagtg 60
tagttcccct gtaagttttt ccatagcttg cactgctaaa tttcgaacaa ggaatttctt 120
gctgctaatc tctaaaaaga tggcatggtt tacaatgatt tttgtttcct tttgattatt 180
atgaacaact gtccatgatt tcgtttaaga atgaagagaa atcactaaac gaactgaata 240
tatttctcgt gccaatatta tctctaattt caaaaaagtt acttttaatg tcggtaatga 300
ctcaaactta ttgatagtgt tttatgttca gataatgccc gatgactttg tcatgcagct 360
ctaatgattt tgagaacgac agcgacttcc gtcccagccg tgccaggtgc tgcctcagat 420
tcagcttatg ccgctcaatt cgctgcgtat atcgcttttc cttatcagtt cgttgatgtc 480
atagcttttg accacgaggg agcttcacgc gagttattga aaaccctga 519

<210> 469
<211> 261
<212> DNA
<213> Escherichia coli

<400> 469
caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatta ttaggaagga 60
aattaatcca attatcgaaa attcaaaaaa tatccaaaaa tagtatactt tattccagaa 120
gagttcaata taatgtttgt cttcaatttt tcttacttca gggtaatata gattgctcat 180
tacattgtga gcttcatctt tatttaattt tctgttgact ccagctctcc gtgataacgg 240
ttttataatt agatgcttat c 261

<210> 470
<211> [illegible]
<212> DNA
<213> Escherichia coli

<400> 470

agatgattgc cgggaacttg ttagcggcac gcaggcggcg gctcgcaccc ttaccctgct 60
ctttacgtac ttctgcgttg atagtaaaca tttctttc 98

<210> 471
<211> 259
<212> DNA
<213> Escherichia coli

<400> 471
tgcgcgaacg aagtcgatgt gctgcagctt cggtttgtac gggtgacgct gtacgtcctg 60
agctttaact ttgatttctt taccgtcaac aacgatggtc agaacttcgc tgtagaattc 120
agctttagct tgcatgtttc tgactttgtc gtgatccagc tcgatagcca gcggcgcttc 180
tttgccatcg tagatgattg cgggaacttt gttagcggca cgcaggcggc ggctcgcacc 240
cttaccctgc tctttacgt 259

<210> 472
<211> 44
<212> DNA
<213> Escherichia coli

<400> 472
aaaaacgccg taaagaaagg atgcaaacat gttaataaaa actcaaattg atccacgta 59
tatattaccc cgcaaaattc ttacaataaa cagg 94

<210> 473
<211> 114
<212> DNA
<213> Escherichia coli

<400> 473
ttaattatta aaatagtgta acgcgattat gtggttatgg cggtaaacat taaataaacc 60
agcgggcagg ggaggtaaag tgaaaaaata aaaagcggat aatcttaata agcaggcgg 120
atacatcgc catccggcac tgatacgagg tttatttcag ctcatcaacc atcg 174

<210> 474
<211> 134
<212> DNA
<213> Escherichia coli

<400> 474
ctgtaaaaac gtcaaaaaga gtgttttatc aacagaagaa tggaggtctg acagatagta 60
gtaatgtaaa aaaatggaga cttaagttga atgaacggga gtaaagcgaa aagactatag 120
agtgaaggag aaattccc 138

<210> 475
<211> 191
<212> DNA
<213> Escherichia coli

<400> 475
tttgttggct taatattcta ttgttatctt tatttataga tgtttatatt gcatgaggtg 60
gttttggaag agaagaatga ggaagatgcg tcgagccaca gaaacgttag ctttacatat 120
agcggaggtg atgtgaaatt aatttacaat agaaataatt tacatatcaa acagttagat 180
gctttttgtc g 191

<210> 476
<211> 245

<212> DNA
<213> Escherichia coli

<400> 476
cggccatcta tacaggaaaa gcctatgtca gaacgtaaaa actcaaaatc acgccgtaat 60
tatcttcgtta aatgttcctg ccaaaactgc acccaagagt cagaacacag ttttttaaga 120
gtacaaaaag gtgccctttt gatctgccct cattgcaaca aagtatttca gacaaatctt 180
aaagcttcag cctgattgat tttattagta acaaagtattt tttatatttt aataatatat 240
ttaaa 245

<210> 477
<211> 419
<212> DNA
<213> Escherichia coli

<400> 477
aaatttttcag gtacccttgtc accatacttt ttttttctgag cattaatgat attttgagct 60
ttttgagtat ctttaacttcc ccacatttggg tggaaagtat tcatatttaaa aggaaggttg 120
aatgattcgt ctttataaat cgccagtggga gaattagtaa aacgatttaaa ttctactaaa 180
ttattaacgt aatcccatat atatttatca ttggtatgaa aaatatgtgc accatattta 240
tgaatctgga tacccttaca gtcctctgtg tacgcatttc cacgcatatg atttcttttc 300
tcaatcacta aaacttttt 319

<210> 478
<211> 149
<212> DNA
<213> Escherichia coli

<400> 478
gcagtgattcg aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga 60
tgacttcgcc cggacgtcag gccgccactt cggtgcgggtt acgtccggct ttctttgctt 120
ttttaacggc caaatctgcc gatttcaac 149

<210> 479
<211> 331
<212> DNA
<213> Escherichia coli

<400> 479
gaaagtattt tcgttattga catcactgga aaatataact tgcttttcat tattaaactc 60
gaagcgcgta ccgtatcttg acaaacattt atcgagctta ccaaattcct gaagaggttt 120
aactacgtat aacatttgcg cgtccttttgc agtaatgccc gtcaaaatcct tgacgggcat 180
tatttatatt aaattaccag tatttcttcg gagtgaagaa tattaccagg tatatttaac 240
acctacgttc gcggacgagt cttgatctac gtcaccacca ccgaggtagt tagcatcggt 300
atagggcgtg aagttcttgg tgaagctaaa 330

<210> 480
<211> 191
<212> DNA
<213> Escherichia coli

<400> 480
ttttttttcca gcaacggagc aaaaggtttg ccccttgtgca gctcagggtt aacccacttta 60
actaagtggc gacgaccccgg agatgtcggt ttacatttaa caactgccat tgtattactc 120
ctcngactta ctcagcgccg ccaacgaagt ccagattctg gcctttctttc agggtgacgt 180
aaagttttttt c 191

<210> 481
<211> 188
<212> DNA
<213> Escherichia coli

<400> 481
tccgtttaac taccagggtg ttaacgactt cgacttcgac ttcaaacagt ttctgcacag 60
cagctttgat ttctgctttg gtcgcgtctt tagcaacttt gagtacgatg gtgttggatt 120
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<211> 172
<212> DNA
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<400> 482
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<211> 266
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<400> 483
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aaaccacaat actcttagcc ctttaacatt taacgcattg tcacgaactc ttctgccgcc 180
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accaggaacc cctgcaacat ttcgtc 266

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<400> 484
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aacaacgata accattgagt tcagcagggc acgcgcggta ccagcctgtg cccaaccgtc 180
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<211> 73
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<213> Escherichia coli

<400> 485
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